

SEQUENCE LISTING

<110> University of Utah Research Foundation
Cogne~~tix~~, Inc.
Olivera, Baldomero M.
McIntosh, J. Michael
Watkins, Maren
Garrett, James E.
Shon, Ki-Joon
Jacobsen, Richard
Jones, Robert M.
Cartier, G. Edward

<120> Omega-Conopeptides

<130> 2314-241

<150> US 09/910,082
<151> 2001-07-23

<150> US 60/219,616
<151> 2000-07-21

<150> US 60/265,888
<151> 2001-02-05

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<170> PatentIn version 3.0

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cgtaactgct gcacttcatg ctcttcatac aaaggaaat gtcggcctcg aaaatgaacc 240
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<211> 76
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<213> Unknown

<220>
<223> unknown Conus species

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1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His His
 20 25 30

Ala Leu Arg Ser Thr Thr Asn Phe Ser Thr Leu Thr Arg Arg Cys Leu
 35 40 45

Ser Pro Gly Ser Arg Cys His Lys Thr Met Arg Asn Cys Cys Thr Ser
 50 55 60

Cys Ser Ser Tyr Lys Gly Lys Cys Arg Pro Arg Lys
 65 70 75

<210> 3

<211> 30

<212> PRT

<213> Unknown

<220>

<223> unknown Conus species

<220>

<221> PEPTIDE

<222> (1)..(30)

<223> Xaa at residue 4 and 28 is Pro or Hyp; Xaa at residue
 22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 3

Cys Leu Ser Xaa Gly Ser Arg Cys His Lys Thr Met Arg Asn Cys Cys
 1 5 10 15

Thr Ser Cys Ser Ser Xaa Lys Gly Lys Cys Arg Xaa Arg Lys
 20 25 30

<210> 4

<211> 283

<212> DNA

<213> Unknown

<220>

<223> unknown Conus species

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aatttctcca cgtcgactcg tcgctgcaaa cctcccgaa gaaaatgtct gaatagaaag 180

aatgaatgtt gcagcaagtt ttgcaatgaa cacctacata tgtgtggata aatggctaaa 240

aactgaataa aagccgcatt gaaaaaaaaaaaaaaa aaa 283

<210> 5

<211> 74

<212> PRT

<213> Unknown

<220>

<223> unknown Conus species

<400> 5

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 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His His
 20 25 30

Ala Leu Arg Ser Thr Thr Asn Phe Ser Thr Ser Thr Arg Arg Cys Lys
 35 40 45

Pro Pro Gly Arg Lys Cys Leu Asn Arg Lys Asn Glu Cys Cys Ser Lys
 50 55 60

Phe Cys Asn Glu His Leu His Met Cys Gly
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<210> 6

<211> 27

<212> PRT

<213> Unknown

<220>

<223> unknown Conus species

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 14 and 22 is Glu or gamma-carboxy Glu;
 Xaa at residue 3 and 4 is Pro or Hyp

<400> 6

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 1 5 10 15

Ser Lys Phe Cys Asn Xaa His Leu His Met Cys
 20 25

<210> 7

<211> 275

<212> DNA

<213> Unknown

<220>

<223> unknown Conus species

<400> 7

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aatctctcca tatcgctcg ctgcaaacct cccagaagaa aatgtctgaa gattaaggat 180

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ataaaaagccg cattgcaaaa aaaaaaaaaa aaaaa 275

<210> 8

<211> 72

<212> PRT

<213> Unknown

<220>

<223> unknown Conus species

<400> 8

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 1 5 10 15

Cys Gln Leu Val Thr Ala Asp Gly Ser Arg Gly Met Gln Lys His Tyr
20 25 30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Ile Ser Ser Arg Cys Lys Pro
35 40 45

Pro Arg Arg Lys Cys Leu Lys Ile Lys Asp Lys Cys Cys Asn Phe Cys
50 55 60

Asn Thr His Leu Asn Met Cys Gly
65 70

<210>	9
<211>	26
<212>	PRT
<213>	Unknown

<220>
<223> unknown Conus species

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<220>
<221> PEPTIDE
<222> (1)..(26)
<223> Xaa at residue 3 and 4 is Pro or Hyp
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<400> 9
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1 5 10 15

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			20					25	

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<212> DNA
<213> Unknown

<220>
<223> unknown Conus species

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aaaaaaaaaaa aaaaaaaaaa 377
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<210> 11
<211> 74
<212> PRT
<213> Unknown

<220>
<223> unknown *Conus* species

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 1 5 10 15

Cys Gln Leu Val Thr Ala Asp Gly Ser Arg Gly Met His Lys His Tyr
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Ser Thr Arg Cys Ala Gly
 35 40 45

Pro Gly Thr Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr Cys Ser Lys
 50 55 60

Arg Thr His Leu Cys His Ser Arg Thr Gly
 65 70

<210> 12

<211> 28

<212> PRT

<213> Unknown

<220>

<223> unknown Conus species

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at
 residue 16 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 12

Cys Ala Gly Xaa Gly Thr Ile Cys Xaa Asn Arg Val Cys Cys Gly Xaa
 1 5 10 15

Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr
 20 25

<210> 13

<211> 323

<212> DNA

<213> Conus arenatus

<400> 13

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actaggcagt gctcggctaa cggtgatct tgtactcgtc atttcactg ctgcagcctc 180

tattgcaata aagattccag tgtatgtgtg gcaacctcat acccgtgagt ggccatgaac 240

ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcattg 300

caataaaaaaa aaaaaaaaaaaa aaa 323

<210> 14

<211> 73

<212> PRT

<213> Conus arenatus

<400> 14

Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr
 20 25 30

Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Ala Asn Gly Gly Ser
 35 40 45

Cys Thr Arg His Phe His Cys Cys Ser Leu Tyr Cys Asn Lys Asp Ser
 50 55 60

Ser Val Cys Val Ala Thr Ser Tyr Pro
 65 70

<210> 15

<211> 33

<212> PRT

<213> Conus arenatus

<220>

<221> PEPTIDE

<222> (1)..(33)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue
 33 is Pro or Hyp; Xaa at residue 19 and 32 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr

<400> 15

Xaa Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys
 1 5 10 15

Ser Leu Xaa Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Xaa
 20 25 30

\Xaa

<210> 16

<211> 326

<212> DNA

<213> Conus arenatus

<400> 16

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ctgaggtcaa ctgacagaaa ctccaagttg accaggacat gcaacactcc cactgaatat 180

tgtactttgc atcgacactg ctgcagcggc tactgccata aaacaatcca ggcatgttca 240

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ctgcattgaa ataaaagccg cattgc 326

<210> 17

<211> 74

<212> PRT

<213> Conus arenatus

<400> 17

Met Lys Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Lys His
 20 25 30

His Ala Leu Arg Ser Thr Asp Arg Asn Ser Lys Leu Thr Arg Thr Cys
 35 40 45

Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Arg His Cys Cys Ser Gly
 50 55 60

Tyr Cys His Lys Thr Ile Gln Ala Cys Ser
 65 70

<210> 18
<211> 28
<212> PRT
<213> Conus arenatus

<220>
<221> PEPTIDE
<222> (1)..(28)
<223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa
at residue 5 is Pro or Hyp; Xaa at residue 8 and 19
is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
O-sulpho-Tyr or O-phospho-Tyr

<400> 18
Thr Cys Asn Thr Xaa Thr Xaa Xaa Cys Thr Leu His Arg His Cys Cys
1 5 10 15

Ser Gly Xaa Cys His Lys Thr Ile Gln Ala Cys Ser
20 25

<210> 19
<211> 332
<212> DNA
<213> Conus arenatus

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ctgaggtcaa ctgacaaaaaa ctccaagttg actaggcagt gcacgcctaa cggtgatct 180
tgttctcgta attttcactg ctgcagcctc tattgcaata aaagtactgg cgtatgtatt 240
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gaggaactgc attgaaataa aagccgcatt gc 332

<210> 20
<211> 79
<212> PRT
<213> Conus arenatus

<400> 20
Met Lys Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Met His
20 25 30

Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys
35 40 45

Thr Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys Ser Leu
50 55 60

Tyr Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Tyr Pro
 65 70 75

<210> 21

<211> 33

<212> PRT

<213> Conus arenatus

<220>

<221> PEPTIDE

<222> (1)..(33)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 and 33 is Pro or Hyp; Xaa at residue 19 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 21

Xaa Cys Thr Xaa Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys
 1 5 10 15

Ser Leu Xaa Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Xaa
 20 25 30

Xaa

<210> 22

<211> 332

<212> DNA

<213> Conus arenatus

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gacaaaaact ccaagttgac caggacatgc aacactcccc ccgaatattt tactttgcat 180

caacactgct gcagcggcta ctgccataaaa acaatccagg catgttcata ataccggta 240

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aaaaccgcat tacaaaaaaaaaaaaaa aa 332

<210> 23

<211> 74

<212> PRT

<213> Conus arenatus

<400> 23

Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Lys His
 20 25 30

His Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Thr Cys
 35 40 45

Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Gln His Cys Cys Ser Gly
 50 55 60

Tyr Cys His Lys Thr Ile Gln Ala Cys Ser
 65 70

<210> 24

<211> 28
 <212> PRT
 <213> Conus arenatus

<220>
 <221> PEPTIDE
 <222> (1)..(28)
 <223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa
 at residue 5 is Pro or Hyp; Xaa at residue 8 and 19
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 24
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 1 5 10 15

Ser Gly Xaa Cys His Lys Thr Ile Gln Ala Cys Ser
 20 25

<210> 25
 <211> 394
 <212> DNA
 <213> Conus arenatus

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 gacaaaaact cccagttgac cagggaatgc acacacctccg gtggagcttg tggtttacct 180
 acacactgct gcgggttttg cgatactgca aacaacagat gtctgtaaag ctggtctggc 240
 gtctgatatt ccccttctgt gctctatcct cttggcctg agtcatccgt acctgtgagt 300
 ggtcatgaac tactcaatac cctctccctct ggaggcttca gaggaactac aatgaaataa 360
 aaccgcatt gcagagaaaa aaaaaaaaaa aaaa 394

<210> 26
 <211> 73
 <212> PRT
 <213> Conus arenatus

<400> 26
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 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Met His
 20 25 30

Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Gln Leu Thr Arg Glu Cys
 35 40 45

Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys Gly Phe
 50 55 60

Cys Asp Thr Ala Asn Asn Arg Cys Leu
 65 70

<210> 27
 <211> 27
 <212> PRT
 <213> Conus arenatus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa
 at residue 4, 5 and 12 is Pro or Hyp

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 1 5 10 15

Gly Phe Cys Asp Thr Ala Asn Asn Arg Cys Leu
 20 25

<210> 28
 <211> 345
 <212> DNA
 <213> Conus arenatus

<220>
 <221> misc_feature
 <222> (1)..(345)
 <223> n may be any nucleotide

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 gacaaaaaact ccaagttgac caggacatgc aacactccca ctgaatattg tactttgcat 180
 caaacactgct gcagcggcca ctgccataaaa acaatccagg catgtgcata ataccggtag 240
 gtggtcatga accactcaat accctctcct ctggaggctt cagaggaact gcattgaaat 300
 aaaaccgcat tgcaatgaan aaaaaaaaaaa aaaaaaaaaaa aaaaa 345

<210> 29
 <211> 74
 <212> PRT
 <213> Conus arenatus

<400> 29
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 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Asn His
 20 25 30

His Val Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Thr Cys
 35 40 45

Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Gln His Cys Cys Ser Gly
 50 55 60

His Cys His Lys Thr Ile Gln Ala Cys Ala
 65 70

<210> 30
 <211> 28
 <212> PRT
 <213> Conus arenatus

<220>
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 <222> (1)..(28)

<223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 5 is Pro or Hyp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 30
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 1 5 10 15
 Ser Gly His Cys His Lys Thr Ile Gln Ala Cys Ala
 20 25

<210> 31
 <211> 322
 <212> DNA
 <213> Conus arenatus

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 actaggcagt gctcgccatat cggtggatat tgtactcttc atattcactg ctgcagcaac 180
 cattgcatta aacctatcg 25 ccgatgtgtg gcaacctgat acccgtgcgt ggtcatgaac 240
 ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcattg 300
 caataaaaaaa aaaaaaaaaaa aa 322

<210> 32
 <211> 70
 <212> PRT
 <213> Conus arenatus

<400> 32
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Thr Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr
 20 25 30

Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Pro Ile Gly Gly Tyr
 35 40 45

Cys Thr Leu His Ile His Cys Cys Ser Asn His Cys Ile Lys Pro Ile
 50 55 60

Gly Arg Cys Val Ala Thr
 65 70

<210> 33
 <211> 30
 <212> PRT
 <213> Conus arenatus

<220>
 <221> PEPTIDE
 <222> (1)..(30)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 and 23 is Pro or Hyp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 33

Xaa Cys Ser Xaa Ile Gly Gly Xaa Cys Thr Leu His Ile His Cys Cys
 1 5 10 15

Ser Asn His Cys Ile Lys Xaa Ile Gly Arg Cys Val Ala Thr
 20 25 30

<210> 34
<211> 318
<212> DNA
<213> Conus arenatus

<400> 34
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actaggcagt gcttcctaa cggatggatat tgtactcttc atattcactg ctgcagcgcac 180
cattgcatta aaccttatcga ccgatgtgtg gcaacctgat acccgggcgt ggtcatgaac 240
ccctcaataac ccttcctct ggaggctca gaggaactgc attgaaataa aaccgcatta 300
aaaaaaaaaaa aaaaaaaaaa 318

<210> 35
<211> 70
<212> PRT
<213> Conus arenatus

<400> 35
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Leu Thr Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr
20 25 30

Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Leu Pro Asn Gly Gly Tyr
35 40 45

Cys Thr Leu His Ile His Cys Cys Ser Asp His Cys Ile Lys Pro Ile
50 55 60

Asp Arg Cys Val Ala Thr
65 70

<210> 36
<211> 30
<212> PRT
<213> Conus arenatus

<220>
<221> PEPTIDE
<222> (1)..(30)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue
4 and 23 is Pro or Hyp; Xaa at residue 8 is Tyr,
125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
or O-phospho-Tyr

<400> 36
Xaa Cys Leu Xaa Asn Gly Gly Xaa Cys Thr Leu His Ile His Cys Cys
1 5 10 15

Ser Asp His Cys Ile Lys Xaa Ile Asp Arg Cys Val Ala Thr
20 25 30

<210> 37
 <211> 374
 <212> DNA
 <213> Conus aurisiacus

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 tccatgtcga ctcgctgcaa gggtaaagga aaaccatgca gtaggatttc gtataactgc 180
 tgcaccgggtt cttgcagatc aggtaaatgt ggctgatcca gcgcctgatc ttcccccttc 240
 tgtgctctat cctttctgc ctgagtccctc cttacctgag agtggtcatg aaccactcat 300
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 aaaaaaaaaa aaaa 374

<210> 38
 <211> 71
 <212> PRT
 <213> Conus aurisiacus

<400> 38
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ser Leu Ser Ser Ala Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
 35 40 45

Lys Gly Lys Pro Cys Ser Arg Ile Ser Tyr Asn Cys Cys Thr Gly Ser
 50 55 60

Cys Arg Ser Gly Lys Cys Gly
 65 70

<210> 39
 <211> 25
 <212> PRT
 <213> Conus aurisiacus

<220>
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 <222> (1)..(25)
 <223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 39
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 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 40
 <211> 380
 <212> DNA
 <213> Conus aurisiacus

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tccatgtcga ctggctgcat ggaagccgga tcttattgct gctctactac gagaatctgc 180
tgcggttttt gcgcattttt cgcaaaaaaa tgtattgact atcccagcaa ctgatctcc 240
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aaaaaaaaaa aaaaaaaaaa 380

<210> 41
<211> 77
<212> PRT
<213> Conus aurisiacus

<400> 41
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ser Leu Arg Ser Lys Thr Lys Leu Ser Met Ser Thr Gly Cys Met Glu
35 40 45

Ala Gly Ser Tyr Cys Gly Ser Thr Thr Arg Ile Cys Cys Gly Phe Cys
50 55 60

Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr Pro Ser Asn
65 70 75

<210> 42
<211> 32
<212> PRT
<213> Conus aurisiacus

<220> .
<221> PEPTIDE
<222> (1)..(32)
<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa
at residue 30 is Pro or Hyp; Xaa at residue 7, 21
and 29 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 42
Cys Met Xaa Ala Gly Ser Xaa Cys Gly Ser Thr Thr Arg Ile Cys Cys
1 5 10 15

Gly Phe Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa Xaa Ser Asn
20 25 30

<210> 43
<211> 373
<212> DNA
<213> Conus aurisiacus

<400> 43
acccaaaacca tcatcaaat gaaactgacg tgggtggta tcgtcgccgt gctgctcctg 60
acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgttccctg 120

agctcggcca ccaaactctc catgtcgact cgctgcaagg ctaaaggaaa accatgcagt 180
 aggattgcgt ataactgctg cacccgttct tgcatcgatcgatgtgg ctgatccagt 240
 gcctgatctt cccccttctg tgctctatcc ttttctgcct gagtcctcct tacctgagag 300
 tggcatgaa ccactcatca cctgctcctc tggaggcccc agaggagcta cattgaaata 360
 aaagccgcat tgc 373

<210> 44
 <211> 71
 <212> PRT
 <213> Conus aurisiacus

<400> 44
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ser Leu Ser Ser Ala Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ala
 35 40 45

Lys Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser
 50 55 60

Cys Arg Ser Gly Lys Cys Gly
 65 70

<210> 45
 <211> 25
 <212> PRT
 <213> Conus aurisiacus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Ty

<400> 45
 Cys Lys Ala Lys Gly Lys Xaa Cys Ser Arg Ile Ala Xaa Asn Cys Cys
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 46
 <211> 379
 <212> DNA
 <213> Conus aurisiacus

<400> 46
 accaaaaacca tcataaaaaat gaaactgacg tgtgtggta tcgtcgccgt gctgctcctg 60
 acgacacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg 120
 aggtcgaaga caaaaactctc catgttaact ttgcgtgcg catcttacgg aaaaccttgt 180
 ggtattgaca acgactgctg caatgcata gatccaggaa gaaatatatg tacgttagctg 240
 atccagcgcc tgatcttccc cttctgtgc tctatcctt tctgcccag tcctccttac 300

ctgagagtgg tcatgaacca ctcatcacct gctccctgga ggcctcagag gagctacaat 360
 gaaataaaaag ccgcattgc 379
 <210> 47
 <211> 72
 <212> PRT
 <213> Conus aurisiacus

<400> 47
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
 20 25 30

Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
 35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Ala Cys
 50 55 60

Asp Pro Gly Arg Asn Ile Cys Thr
 65 70

<210> 48
 <211> 26
 <212> PRT
 <213> Conus aurisiacus

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at
 residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 48
 Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn
 1 5 10 15

Ala Cys Asp Xaa Gly Arg Asn Ile Cys Thr
 20 25

<210> 49
 <211> 382
 <212> DNA
 <213> Conus bullatus

<400> 49
 accaaaaacca tcatcaaaat gaaactgacg tgtgtggcga tcgtcgccgt gctgctcctg 60
 acggcctgtc agctcattac agctgaagac tccagaggta cgcatgagca tcttgcctg 120
 aagtgcacct ccaaagtctc caagtcgact agctgcattgg aagccggatc ttattgcgga 180

cctgctacta cgaaaatctg ctgcgatttt tgcaagtccat tcagcgatag atgttatgaac 240

aatcccaaca attgatcttc ccccttgtgt gctccatcct tttctgcctg agtcctcctt 300

acctgagagt ggtcatgaac cactcatcac ctactcctct ggaggctca gaggagctac 360

attgaaataa aagccgcatt gc 382

<210> 50

<211> 78
 <212> PRT
 <213> Conus bullatus

<400> 50
 Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu
 20 25 30

Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Glu
 35 40 45

Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr Lys Ile Cys Cys Asp Phe
 50 55 60

Cys Ser Pro Phe Ser Asp Arg Cys Met Asn Asn Pro Asn Asn
 65 70 75

<210> 51
 <211> 36
 <212> PRT
 <213> Conus bullatus

<220>
 <221> PEPTIDE
 <222> (1)..(36)
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa
 at residue 13, 25 and 34 is Pro or Hyp; Xaa at
 residue 10 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 51
 Ser Thr Ser Cys Met Xaa Ala Gly Ser Xaa Cys Gly Xaa Ala Thr Thr
 1 5 10 15

Lys Ile Cys Cys Asp Phe Cys Ser Xaa Phe Ser Asp Arg Cys Met Asn
 20 25 30

Asn Xaa Asn Asn
 35

<210> 52
 <211> 400
 <212> DNA
 <213> Conus bullatus

<400> 52
 accaaaacca tcatcaaaat gaaactgacg tgtgtggta tcgtcgccgt gctgctcctg 60
 acggcctgtc agtcattac agctgaagac tccagaggta cgcagttgca tcgtgccctg 120
 aggaaggcca ccaaacaccc tgtgtcgact cgctgcatta ctccaggaac acgatgtaa 180
 gttccgagcc aatgctgcag aggtccttgc aagaacggtc gttgtactcc atccccttct 240
 gaatggtaaa tgtggttgat ccagcgccgt atcttcccccc ttctgtgc tccatccttt 300
 tctgccttag tcctccttac ctgagagtgg tcatgaacca ctcatcacct actccccctgg 360
 aggcttcaga ggagctacat tgaaataaaa gccgcattgc 400

<210> 53
 <211> 76

<212> PRT

<213> Conus bullatus

<400> 53

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg
20 25 30Ala Leu Arg Lys Ala Thr Lys His Pro Val Ser Thr Arg Cys Ile Thr
35 40 45Pro Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg Gly Pro Cys
50 55 60Lys Asn Gly Arg Cys Thr Pro Ser Pro Ser Glu Trp
65 70 75

<210> 54

<211> 31

<212> PRT

<213> Conus bullatus

<220>

<221> PEPTIDE

<222> (1)..(31)

<223> Xaa at residue 30 is Glu or gamma-carboxy Glu; Xaa
at residue 4, 11, 18, 26 and 28 is Pro or Hyp; Xaa
at residue 31is Trp or Bromo-Trp

<400> 54

Cys Ile Thr Xaa Gly Thr Ala Cys Lys Val Xaa Ser Gln Cys Cys Arg
1 5 10 15Gly Xaa Cys Lys Asn Gly Arg Cys Thr Xaa Ser Xaa Ser Xaa Xaa
20 25 30

<210> 55

<211> 379

<212> DNA

<213> Conus bullatus

<400> 55

acccaaaaccca tcatcaaaat gaaaactgacg tgtgtggcga tcgtcgccgt gctgctcctg 60

acggcctgtc agtcattac agctgaggac tccagagata cgcagaagca tcgtgccctg 120

aggtcggaca ccaaactctc catgttgact ttgcgctgcg caacttacgg aaaaccttgt 180

gttattcaaa acgactgctg caatacatgc gatccagcca gaaggacatg tacgttagctg 240

atccggcgtc ttgatcctcc gcttctgtgc tccatcttt ctgcctgagt cctccttacc 300

tgagagtggc catgaaccac tcatcaccta ctccctctgga ggctttagag gagctacatt 360

gaaataaaag ccgcattgc 379

<210> 56

<211> 72

<212> PRT

<213> Conus bullatus

<400> 56

Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Asp Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
 35 40 45

Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn Thr Cys
 50 55 60

Asp Pro Ala Arg Arg Thr Cys Thr
 65 70

<210> 57

<211> 26

<212> PRT

<213> Conus bullatus

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at
 residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 57

Cys Ala Thr Xaa Gly Lys Xaa Cys Gly Ile Gln Asn Asp Cys Cys Asn
 1 5 10 15

Thr Cys Asp Xaa Ala Arg Arg Thr Cys Thr
 20 25

<210> 58

<211> 373

<212> DNA

<213> Conus bullatus

<400> 58

accaaaaacca tcataaaaaat gaaaactgacg tgggtggcga tcgtcgccgt gctgctccctg 60

acggcctgtc agtcattttt acgttgtttttt tccagaggta cgcaggatgtca tcgtgccttg 120

aggaagacca ccaaactctc cttgtcgact cgctgcaagg gtccaggagc atcatgtata 180

aggattgcgt ataactgctg caagtattttt tgcagaaatg gtaaatgtgg ctgatccagc 240

gcctgatctt ccccccttgtt tgctccatcc ttttctgcct gagtcctcct tacctgagag 300

tggtcatgaa ccactcatca cctactcctc tggaggcttc agaggagcta cattgaaata 360

aaagccgcat tgc 373

<210> 59

<211> 71

<212> PRT

<213> Conus bullatus

<400> 59

Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg
 20 25 30

Ala Leu Arg Lys Thr Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Gly
 35 40 45

Pro Gly Ala Ser Cys Ile Arg Ile Ala Tyr Asn Cys Cys Lys Tyr Ser
 50 55 60

Cys Arg Asn Gly Lys Cys Gly
 65 70

<210> 60
<211> 25
<212> PRT
<213> Conus bullatus

<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa at residue 4 is Pro or Hyp; Xaa at residue 13
and 18 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
O-sulpho-Tyr or O-phospho-Tyr

<400> 60
Cys Lys Gly Xaa Gly Ala Ser Cys Ile Arg Ile Ala Xaa Asn Cys Cys
1 5 10 15

Lys Xaa Ser Cys Arg Asn Gly Lys Cys
20 25

<210> 61
<211> 382
<212> DNA
<213> Conus bullatus

<400> 61
atcaaaaacca tcatcaaaat gaaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
acggcctgtc agctcattac agctgaagac tccagaggta cgcatttttttgcggatc ttattgcgga 120
aagtgcacctt cc当地gactt caagtcgact agctgcattgg cagccggatc ttattgcgga 180
cctgctacta cgaatatctg ctgcgatttt tgcatgtccat tcagcgatag atgtatgaaa 240
aagcccaaca attgatcttc ccccttctgt gctctatcct tttctgcctg agtcctcctt 300
acctgagagt ggtcatgaac cactcatcac ctactcctct ggaggctca gaggagctac 360
attgaaataa aagccgcatt gc 382

<210> 62
<211> 78
<212> PRT
<213> Conus bullatus

<400> 62
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu
20 25 30

Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Ala
35 40 45

Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr Asn Ile Cys Cys Asp Phe
 50 55 60

Cys Ser Pro Phe Ser Asp Arg Cys Met Lys Lys Pro Asn Asn
 65 70 75

<210> 63
 <211> 36
 <212> PRT
 <213> Conus bullatus

<220>
 <221> PEPTIDE
 <222> (1)..(36)
 <223> Xaa at residue 13, 25 and 34 is Pro or Hyp; Xaa at
 residue 10 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 63
 Ser Thr Ser Cys Met Ala Ala Gly Ser Xaa Cys Gly Xaa Ala Thr Thr
 1 5 10 15

Asn Ile Cys Cys Asp Phe Cys Ser Xaa Phe Ser Asp Arg Cys Met Lys
 20 25 30

Lys Xaa Asn Asn
 35

<210> 64
 <211> 373
 <212> DNA
 <213> Conus bullatus

<400> 64
 accaaaaacca tcatcaaaat gaaaactgacg tgtgtggta tcgtcgccgt gctgctcctg 60
 acggcctgtc agtcattat agctgaggac tccagaggta cgcatggca tcgtgccctg 120
 aggaaggcca ccaaactctc cgtgtcgact cgctgcaaga gtaaaggatc atcatgtcat 180
 aggacttcgt atgactgctg cacgggttct tgtagaaatg gtatgtgg ctgatccagc 240
 gcctgatctt ccccattctg tgctccatcc ttttctgcct gagtcctcct tacctgagag 300
 tggtcatgaa ccactcatca cctactcctc tggaggcttc agaggagcta cattgaaata 360
 aaagccgcat tgc 373

<210> 65
 <211> 71
 <212> PRT
 <213> Conus bullatus

<400> 65
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Ile Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg
 20 25 30

Ala Leu Arg Lys Ala Thr Lys Leu Ser Val Ser Thr Arg Cys Lys Ser
 35 40 45

Lys Gly Ser Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser
 50 55 60

Cys Arg Asn Gly Arg Cys Gly
65 70

<210> 66
<211> 25
<212> PRT
<213> Conus bullatus

<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 66
Cys Lys Ser Lys Gly Ser Ser Cys His Arg Thr Ser Xaa Asp Cys Cys
1 5 10 15

Thr Gly Ser Cys Arg Asn Gly Arg Cys
20 25

<210> 67
<211> 321
<212> DNA
<213> Conus characteristicus

<400> 67
ggatccatga aactgacgtg cgtggtgatc atcgccgtgc tggccctgac ggcctgtcaa 60
ctcattacag gtgagcagaa ggaccatgct ctgaggtcaa ctgacaaaaa ctccaagttg 120
actaggcagt gctcggctaa cggtggatct tgtactcgtc attttcactg ctgcagcctc 180
tattgcaata aagattccag tgtatgtgtg gcaacctcat acccgtgagt ggccatgaac 240
ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcatta 300
caaaaaaaaaaaa aaaaaaaaaa a 321

<210> 68
<211> 73
<212> PRT
<213> Conus characteristicus

<400> 68
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr
20 25 30

Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Ala Asn Gly Gly Ser
35 40 45

Cys Thr Arg His Phe His Cys Cys Ser Leu Tyr Cys Asn Lys Asp Ser
50 55 60

Ser Val Cys Val Ala Thr Ser Tyr Pro
65 70

<210> 69
<211> 33
<212> PRT
<213> Conus characteristicus

<220>
 <221> PEPTIDE
 <222> (1)..(33)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue
 33 is Pro or Hyp; Xaa at residue 19 and 32 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr

<400> 69
 Xaa Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys
 1 5 10 15

Ser Leu Xaa Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Xaa
 20 25 30

Xaa

<210> 70
 <211> 26
 <212> PRT
 <213> Conus catus

<400> 70
 Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Arg Cys Gly
 20 25

<210> 71
 <211> 25
 <212> PRT
 <213> Conus catus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 71
 Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Xaa Asp Cys Cys
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Arg Cys
 20 25

<210> 72
 <211> 229
 <212> DNA
 <213> Conus catus

<400> 72
 tcgactcgct gccagggtag aggagcatca tgcgttaaga ctatgtataa ctgctgcagc 60
 gttcttgca acagaggtag ttgtggctga tccggcgccct gatcttcccc cttccgtgct 120
 ctatcctttt ctgcctgatt ctccttacc tgagagcggt catgaaccac tcacacac 180
 ctcctctgga ggcctcagag gagtacatt gaaataaaag ccgcattgc 229

<210> 73
 <211> 29

<212> PRT

<213> Conus catus

<400> 73

Ser Thr Arg Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Tyr
1 5 10 15Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Ser Cys Gly
20 25

<210> 74

<211> 25

<212> PRT

<213> Conus catus

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 74

Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Xaa Asn Cys Cys
1 5 10 15Ser Gly Ser Cys Asn Arg Gly Ser Cys
20 25

<210> 75

<211> 235

<212> DNA

<213> Conus catus

<400> 75

tcgacacgcgt gcttgcctgc cggagagtct tgcctttta gtaggattag atgctgcgg 60

acttgcaggc cagtctaaa gtcatgtgtg agctgatcca gctgctgatc ttccctcctcc 120

tgtgctccat cctttctgc ctgagtcctc cttatctgag agtggcatg aaccactcac 180

cacctactct tctggaggct tcagaggagc tacagtgaaa taaaagccgc attgc 235

<210> 76

<211> 31

<212> PRT

<213> Conus catus

<400> 76

Ser Thr Arg Cys Leu Pro Ala Gly Glu Ser Cys Leu Phe Ser Arg Ile
1 5 10 15Arg Cys Cys Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser
20 25 30

<210> 77

<211> 28

<212> PRT

<213> Conus catus

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa
at residue 3 is Pro or Hyp

<400> 77
Cys Leu Xaa Ala Gly Xaa Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
1 5 10 15

Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser
20 25

<210> 78
<211> 227
<212> DNA
<213> Conus catus

<400> 78
tcgacacgct gccagggtag aggaggacca tgtactaagg ctgtgtttaa ctgctgcagc 60
ggttcttgca acagaggtag atgtggctga tccagcgccc gatcttcccc cttctgtgct 120
ctatcctttt ctgcctgagt cctccttact gagagtagtc atgaaccact catcacctac 180
tcctctggag gcctcagaga gctacattga aataaaagcc gcattgc 227

<210> 79
<211> 29
<212> PRT
<213> Conus catus

<400> 79
Ser Thr Arg Cys Gln Gly Arg Gly Gly Pro Cys Thr Lys Ala Val Phe
1 5 10 15

Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Arg Cys Gly
20 25

<210> 80
<211> 25
<212> PRT
<213> Conus catus

<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa at residue 7 is Pro or Hyp

<400> 80
Cys Gln Gly Arg Gly Xaa Cys Thr Lys Ala Val Phe Asn Cys Cys
1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Arg Cys
20 25

<210> 81
<211> 236
<212> DNA
<213> Conus catus

<400> 81
ttaactttgc gctgcgcaac ttacggaaaa ccttgtggta ttcaaaaacga ctgctgcaat 60
acatgcgatc cagccagaaa gacatgtacg tagctgatcc ggcgtctgat ctccccccctt 120
ctgtgctcta tcctttctg cctgagtcct ccttacctga gagtggtcat gaaccactca 180
tcacctgctc ctctggaggc ctgggggag ctacattgaa ataaaagccg cattgc 236

<210> 82

<211> 30
<212> PRT
<213> Conus catus

<400> 82
Leu Thr Leu Arg Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn
1 5 10 15
Asp Cys Cys Asn Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr
20 25 30

<210> 83
<211> 26
<212> PRT
<213> Conus catus

<220>
<221> PEPTIDE
<222> (1)..(26)
<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at
residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 83
Cys Ala Thr Xaa Gly Lys Xaa Cys Gly Ile Gln Asn Asp Cys Cys Asn
1 5 10 15
Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr
20 25

<210> 84
<211> 229
<212> DNA
<213> Conus catus

<400> 84
tcgactcgct gccgggttag aggaggacca tgtactaagg ctatgtttaa ctgctgcagc 60
ggttcttgca acagaggttag atgtggctga tccagcgcct gatctcccc cttctgtgct 120
ctatcctttt ctgcctgagt ctccttaac tgagagtagt catgaaccac tcatacaccta 180
ctcctctgga ggcctcagag aagcatcatt gaaataaaag ccgcattgc 229

<210> 85
<211> 29
<212> PRT
<213> Conus catus

<400> 85
Ser Thr Arg Cys Arg Gly Arg Gly Pro Cys Thr Lys Ala Met Phe
1 5 10 15

Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Arg Cys Gly
20 25

<210> 86
<211> 25
<212> PRT
<213> Conus catus

<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa at residue 7 is Pro or Hyp

<400> 86
Cys Arg Gly Arg Gly Gly Xaa Cys Thr Lys Ala Met Phe Asn Cys Cys
1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Arg Cys
20 25

<210> 87
<211> 374
<212> DNA
<213> Conus circumcisus

<400> 87
acccaaaacca tcatcaaaat gaaaactgacg tgtgtggta tcgtcgccgt gctgctcctg 60
acgacacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg 120
aggtcggaca ccaaactccc catgtcgact cgctgcaagg gtaaaggagc atcatgtcgt 180
aagactatgt ataactgctg cagcggttct tgtagcaacg gttagatgtgg ctgatccagc 240
gcctgatctt cccccttctg ctgctctatc cttttctgcc tgagtcctcc ttacctgaga 300
gctggtcatg aaccactcat cacctgctcc tctggaggcc cagaggagct acattgaaat 360
aaaagccgca ttgc 374

<210> 88
<211> 71
<212> PRT
<213> Conus circumcisus

<400> 88
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Pro Met Ser Thr Arg Cys Lys Gly
35 40 45

Lys Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys Ser Gly Ser
50 55 60

Cys Ser Asn Gly Arg Cys Gly
65 70

<210> 89
<211> 25
<212> PRT
<213> Conus circumcisus

<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 89
Cys Lys Gly Lys Gly Ala Ser Cys Arg Lys Thr Met Xaa Asn Cys Cys
1 5 10 15

Ser Gly Ser Cys Ser Asn Gly Arg Cys
20 25

<210> 90
 <211> 379
 <212> DNA
 <213> Conus circumcisus

<400> 90
 accaaaaacca tcatcaaaat gaaaactgacg tgggtggta tcgtcgccgt gctgctcctg 60
 acgacacctgc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcggcca ccaaagtctc caagtcgact agctgcattgg aagccggatc ttattgccgc 180
 tctactacga gaacctgctg cggttattgc tcttatttca gcaaaaaatg tattgacttt 240
 cccagcaact gatcttcccc ctactgtgct ctatccttt ctgcctgagt ctccttacc 300
 tgagagtggc catgaaccac tcatcacccct actcctctgg aggcccagag gagctacatt 360
 gaaataaaag ccgcattgc 379

<210> 91
 <211> 77
 <212> PRT
 <213> Conus circumcisus

<400> 91
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Ala Thr Lys Val Ser Lys Ser Thr Ser Cys Met Glu
 35 40 45

Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg Thr Cys Cys Gly Tyr Cys
 50 55 60

Ser Tyr Phe Ser Lys Lys Cys Ile Asp Phe Pro Ser Asn
 65 70 75

<210> 92
 <211> 35
 <212> PRT
 <213> Conus circumcisus

<220>
 <221> PEPTIDE
 <222> (1)..(35)
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at
 residue 33 is Pro or Hyp; Xaa at residue 10, 21 and
 24 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 92
 Ser Thr Ser Cys Met Xaa Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg
 1 5 10 15

Thr Cys Cys Gly Xaa Cys Ser Xaa Phe Ser Lys Lys Cys Ile Asp Phe
 20 25 30

Xaa Ser Asn
 35

<210> 93
 <211> 379
 <212> DNA
 <213> Conus circumcisus

<400> 93
 accaaaaacca tcatcaaaat gaaaactgacg tgtgtggta tcgtcgccgt gctgctcctg 60
 acgacacctgc aactcatcac agctgatgac tccagaggta cgccaggagca tcgtgccctg 120
 aggtcggaca ccaaactccc catgtcgact cgctgcaaga gtaaaggagc aaaatgttca 180
 aggcttatgt atgactgctg cagcggtctc tgccagcaggacttcaggtag atgtggctga 240
 tccagcgccct gatcttcccc cttctgctgc tctatccttt tctgcctgag tcctccttac 300
 ctgagagtggtt tcatgaacca ctcatcacct actcctctgg aggcccagag gagctacatt 360
 gaaataaaag ccgcattgc 379

<210> 94
 <211> 73
 <212> PRT
 <213> Conus circumcisus

<400> 94
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Pro Met Ser Thr Arg Cys Lys Ser
 35 40 45

Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys Ser Gly Ser
 50 55 60

Cys Ser Arg Tyr Ser Gly Arg Cys Gly
 65 70

<210> 95
 <211> 27
 <212> PRT
 <213> Conus circumcisus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 13 and 23 is Tyr, 125I-Tyr,
 mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr

<400> 95
 Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Xaa Asp Cys Cys
 1 5 10 15

Ser Gly Ser Cys Ser Arg Xaa Ser Gly Arg Cys
 20 25

<210> 96
 <211> 379
 <212> DNA
 <213> Conus circumcisus

<400> 96
 accaaaaacca tcatcaaaat gaaaactgacg tgtgtggta tcgtcgccgt gctgctcctg 60
 acgacctgtc aactcatcac agctgatgac tccagaggta cgcaagaagca tcgttccctg 120
 acgtcgccca ccaaagtctc caagtcgact ggctgcatga aagccggatc ttattgccgc 180
 tctactacga gaacttgcgt cggttattgc gcttatttcg gcaaaaaatg tattgactat 240
 cccagcaact gatctcccc ctactgtgct ctatcctttt ctgcctaagt ctccttacc 300
 tgagagtgg catgaaccac tcatcaccc actcctctgg aggcccagag gagctacatt 360
 gaaataaaag ccgcattgc 379

<210> 97
<211> 77
<212> PRT
<213> Conus circumcisus

<400> 97
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ser Leu Thr Ser Ala Thr Lys Val Ser Lys Ser Thr Gly Cys Met Lys
 35 40 45

Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg Thr Cys Cys Gly Tyr Cys
 50 55 60

Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr Pro Ser Asn
 65 70 75

<210> 98
<211> 35
<212> PRT
<213> Conus circumcisus

<220>
<221> PEPTIDE
<222> (1)..(35)
<223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10,
 21, 24 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 98
 Ser Thr Gly Cys Met Lys Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg
 1 5 10 15

Thr Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa
 20 25 30

Xaa Ser Asn
 35

<210> 99
<211> 362
<212> DNA
<213> Conus consors

<400> 99
 atgaaaactga cgtgtgtggt gatcgctgcc gtgctgctcc tgacggcctg tcaactcctc 60

acagctgatg actccagagg tacgcagaag catcgtgcc tgaagtctta caccaaactc 120
 tccatgttaa ctggcgctg cgcatcttac ggaaaacctt gtggattga caacgactgc 180
 tgcaatacat gcgatccagc cagaaagaca tgtacgtac tgatccggcg tctgatcttc 240
 ccccttctgt gctctatcct tttctgcctg agtcctcctt acctgagagt ggtcatgaac 300
 cactcatcac cttagtcctc tggaggcttc agaggagcta caatgaaata aaagcgcatt 360
 gc 362

<210> 100
 <211> 72
 <212> PRT
 <213> Conus consors

<400> 100
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Lys Ser Tyr Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
 35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Thr Cys
 50 55 60

Asp Pro Ala Arg Lys Thr Cys Thr
 65 70

<210> 101
 <211> 26
 <212> PRT
 <213> Conus consors

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at
 residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 101
 Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn
 1 5 10 15

Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr
 20 25

<210> 102
 <211> 237
 <212> DNA
 <213> Conus consors

<400> 102
 atgaaactga cgtgtgttgt gatcgctgcc gtgctgctcc tgacggcctg tcaactcctc 60
 acagctgatg actccagagg tacgcagaag catcgtgcc tggatcgga caccaaactc 120
 tccatgtcga ctcgctgcaa gggtagatggaa aaaccatgca gttaggattgc gtataactgc 180

tgcaccgggtt cttgcagatc aggtaaatgt ggctgatcca ggcgcctgatc tccccc 237
 <210> 103
 <211> 71
 <212> PRT
 <213> Conus consors

<400> 103
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
 35 40 45

Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser
 50 55 60

Cys Arg Ser Gly Lys Cys Gly
 65 70

<210> 104
 <211> 25
 <212> PRT
 <213> Conus consors

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 104
 Cys Lys Gly Arg Gly Lys Xaa Cys Ser Arg Ile Ala Xaa Asn Cys Cys
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 105
 <211> 320
 <212> DNA
 <213> Conus consors

<400> 105
 atgaaaactga cgtgtgtggatgcgtcgcc gtgctgctcc tgacggctgtcaactcatc 60
 acagctgatg actccaaagg tacgcagaag catcgttccc tgaggtcgac caccaaagtgc 120
 tccaaaggcga ctgactgcat tgaagccgga aattattgcg gacctactgt tatgaaaatc 180
 tgctgcggct tttgcagtcc atacagcaaa atatgtatga actatccccaaattgtatct 240
 tcccccttct gtgctctatc cttttctgcc tgagtcctcc ttacctgaga gtggtcata 300
 accactcatc acctcgatccc 320

<210> 106
 <211> 78
 <212> PRT
 <213> Conus consors

<400> 106
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Lys Gly Thr Gln Lys His Arg
 20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ala Thr Asp Cys Ile Glu
 35 40 45

Ala Gly Asn Tyr Cys Gly Pro Thr Val Met Lys Ile Cys Cys Gly Phe
 50 55 60

Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn Tyr Pro Gln Asn
 65 70 75

<210> 107
<211> 36
<212> PRT
<213> Conus consors

<220>
<221> PEPTIDE
<222> (1)..(36)
<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at
 residue 13, 25 and 34 is Pro or Hyp; Xaa at residue
 10, 26 and 33 is Tyr, 125 I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 107
 Ala Thr Asp Cys Ile Xaa Ala Gly Asn Xaa Cys Gly Xaa Thr Val Met
 1 5 10 15

Lys Ile Cys Cys Gly Phe Cys Ser Xaa Xaa Ser Lys Ile Cys Met Asn
 20 25 30

Xaa Xaa Gln Asn
 35

<210> 108
<211> 321
<212> DNA
<213> Conus consors

<400> 108
 atgaaaactga cgtgtgtggc gatcgctgcc gtgcgtgcctcc tgacggcctg tcaactcctc 60
 acagctgatg actccagagg tacgcagaag catcggtccc tgaggtcgga caccaaactc
 tccatgtcga ctcgctgcaa aggtaaagga gcatcatgta caaggcttat gtatgactgc 120
 tgccacgggtt cttgcagcag cagcaagggtt agatgtggct gatccggcgc ctgatcttcc
 cccttctgtg ctctatcctt ttctgcctga gtcctcctta cctgagaggtt ggtcatgaac
 cactcatcac ctgctccccct g 180
 240
 300
 321

<210> 109
<211> 73
<212> PRT
<213> Conus consors

<400> 109
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
 35 40 45

Lys Gly Ala Ser Cys Thr Arg Leu Met Tyr Asp Cys Cys His Gly Ser
 50 55 60

Cys Ser Ser Ser Lys Gly Arg Cys Gly
 65 70

<210> 110

<211> 27

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 110

Cys Lys Gly Lys Gly Ala Ser Cys Thr Arg Leu Met Xaa Asp Cys Cys
 1 5 10 15

His Gly Ser Cys Ser Ser Ser Lys Gly Arg Cys
 20 25

<210> 111

<211> 292

<212> DNA

<213> Conus consors

<400> 111

ggatccataga aactgacgtg catggtgatc gtcgccgtgc tgctcctgac ggcctgtcaa 60
 ctcatcacag ctgatgactc cagaggtacg cagaaggcatc gtgcctctgag gtcggacacc 120

aaactctcca tgtcaactcg ctgcaagggt aaaggagcat catgtcatag gacttcgtat 180

gactgctgca ccgggttcttg caacagaggt aaatgtggct gatccggcgc ctgatcttcc 240

cccttctgtg ctctatcctt ttctgcctga gtcatccata cctgtgctcg ag 292

<210> 112

<211> 71

<212> PRT

<213> Conus consors

<400> 112

Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
 35 40 45

Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser
 50 55 60

Cys Asn Arg Gly Lys Cys Gly
 65 70

<210> 113

<211> 25

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 113

Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Xaa Asp Cys Cys
1 5 10 15Thr Gly Ser Cys Asn Arg Gly Lys Cys
20 25

<210> 114

<211> 299

<212> DNA

<213> Conus consors

<400> 114

ggatccatga aactgacgtg cgtggtgatc gtcgcgtgc tgctcctgac gcgcgtcaa 60

ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgcctgaa gtcggacacc 120

aaactctcca tgttaacttt gcgcgcgca tcttacggaa aaccttgtgg tatttacaac 180

gactgctgca atacatgcga tccagccaga aagacatgta cgtagctgat ccggcgtctg 240

atcttccccc ttctgtgctc tatcctttc tgcctgagtc atccataacct gtgctcgag 299

<210> 115

<211> 72

<212> PRT

<213> Conus consors

<400> 115

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30Ala Leu Lys Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
35 40 45Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Thr Cys
50 55 60Asp Pro Ala Arg Lys Thr Cys Thr
65 70

<210> 116

<211> 26

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at

residue 4 and 11 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 116
Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn
1 5 10 15

Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr
20 25

<210> 117
<211> 434
<212> DNA
<213> Conus consors

<220>
<221> misc_feature
<222> (1)..(434)
<223> n may be any nucleotide

<400> 117
ggatccatga aactgacgtg tgtggtgatc gtcgcgtgc tgctcctgac ggcctgtcaa 60
ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgcctgag gtcggacacc 120
aaactctcca tgtcgactcg ctgcaagggt acaggaaaac catgcagtag gtttgcgtat 180
aactgctgca ccgggttcttg cagatcaggt aaatgtggct gatccagtgc ctgatcttcc 240
cccttctgtg ctctatcctt ttctgcctga gtccctccta cctgagagtg gtcatgaacc 300
actcatcacc tgctcctctg gaggcttcag aggagctaca ttgaaataaa agccgcattg 360
cantgnanaa aannnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nngaaaaaaa 420
aaaaaaaaaaa aaaa 434

<210> 118
<211> 71
<212> PRT
<213> Conus consors

<400> 118
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
35 40 45

Thr Gly Lys Pro Cys Ser Arg Val Ala Tyr Asn Cys Cys Thr Gly Ser
50 55 60

Cys Arg Ser Gly Lys Cys Gly
65 70

<210> 119
<211> 25
<212> PRT
<213> Conus consors

<220>
<221> PEPTIDE

<222> (1)..(25)
 <223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 119
 Cys Lys Gly Thr Gly Lys Xaa Cys Ser Arg Val Ala Xaa Asn Cys Cys
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 120
 <211> 393
 <212> DNA
 <213> Conus consors

<400> 120
 ggatccatga aactgacgtg catggtgatc gtcgccgtgc tgctcctgac ggcctgtcaa 60
 ctcatcacag ctgatgactc cagaggtacg cagaagcatc gttccctgag gtcgaccacc 120
 aaagtctcca agtcgactag ctgcatgaaa gccgggtctt attgccgctc tactacgaga 180
 acctgctgca gttattgcgc ttatttcggc aaatttgtta ttgactttcc cagcaactga 240
 tctccccct actgtgctct atcctttct gcctctgcct gagtcctcct tacctgagag 300
 tggtcatgaa ccactcatca cctgctcccc tggaggcctc agaggagcta caatgaaata 360
 aaagccgcat tgcaaaaaaaa aaaaaaaaaa aaa 393

<210> 121
 <211> 77
 <212> PRT
 <213> Conus consors

<400> 121
 Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys
 35 40 45

Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg Thr Cys Cys Gly Tyr Cys
 50 55 60

Ala Tyr Phe Gly Lys Phe Cys Ile Asp Phe Pro Ser Asn
 65 70 75

<210> 122
 <211> 35
 <212> PRT
 <213> Conus consors

<220>
 <221> PEPTIDE
 <222> (1)..(35)
 <223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10,
 21 and 24 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 122
 Ser Thr Ser Cys Met Lys Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg
 1 5 10 15

Thr Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Phe Cys Ile Asp Phe
 20 25 30

Xaa Ser Asn
 35

<210> 123
 <211> 361
 <212> DNA
 <213> Conus dalli

<400> 123
 accaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgttcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaagta cgccagaagca tcgtgctctg 120
 aggtcgacca tcaaacactc catgttactt aggagctgca cgcctcccg aggaccttgt 180
 ggttattata atgactgctg cagtcataa tgcaatataa gcagaaataa atgcgagtag 240
 ctgatccggc atctgatctt ccccttctgt gctcgcccta acctgagagt ggtcatgaac 300
 catcatcacc tactcctctg gaggcttcag aggagctaca tggaaataaa agccgcattg 360
 c 361

<210> 124
 <211> 73
 <212> PRT
 <213> Conus dalli

<400> 124
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Ser Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Thr Ile Lys His Ser Met Leu Thr Arg Ser Cys Thr
 35 40 45

Pro Pro Gly Gly Pro Cys Gly Tyr Tyr Asn Asp Cys Cys Ser His Gln
 50 55 60

Cys Asn Ile Ser Arg Asn Lys Cys Glu
 65 70

<210> 125
 <211> 28
 <212> PRT
 <213> Conus dalli

<220>
 <221> PEPTIDE
 <222> (1)..(28)
 <223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa
 at residue 4, 5 and 8 is Pro or Hyp; Xaa at residue
 11 and 12 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 125

Ser Cys Thr Xaa Xaa Gly Gly Xaa Cys Gly Xaa Xaa Asn Asp Cys Cys
 1 5 10 15

Ser His Gln Cys Asn Ile Ser Arg Asn Lys Cys Xaa
 20 25

<210> 126
 <211> 350
 <212> DNA
 <213> Conus distans

<400> 126
 accaaaaacca tcatcaaaaat gaaaactgacg tgctgttga tcatcgccgt gctgttcctg 60
 acggcctgtc aactcactag agggaaagctg gagcgtcctg ttctgagggtc gagcgaccaa 120
 acctccgggt caacgaagag atgcgaagat cctggtaaac cttgcggaaag tgatcattcc 180
 tgctgcggcg gtagttgcaa ccacaacgtc tgccctgaa gctggcttgg catctgacca 240
 ttcccccttc gtactctatac tctattgcct gagtcatctt tacctgtgag tggtcatgaa 300
 tctctcaata ccttctcccc tggaggcttc agaagaacta gattgaaata 350

<210> 127
 <211> 66
 <212> PRT
 <213> Conus distans

<400> 127
 Met Lys Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Thr Arg Gly Lys Leu Glu Arg Pro Val Leu Arg Ser Ser
 20 25 30

Asp Gln Thr Ser Gly Ser Thr Lys Arg Cys Glu Asp Pro Gly Glu Pro
 35 40 45

Cys Gly Ser Asp His Ser Cys Cys Gly Gly Ser Cys Asn His Asn Val
 50 55 60

Cys Ala
 65

<210> 128
 <211> 25
 <212> PRT
 <213> Conus distans

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 2 and 6 is Glu or gamma-carboxy Glu;
 Xaa at residue 4 and 7 is Pro or Hyp

<400> 128
 Cys Xaa Asp Xaa Gly Xaa Xaa Cys Gly Ser Asp His Ser Cys Cys Gly
 1 5 10 15

Gly Ser Cys Asn His Asn Val Cys Ala
 20 25

<210> 129
 <211> 309
 <212> DNA

<213> Conus ermineus

<400> 129
atgaaactga cgtgtgtggt gatcgctgcc gtcgtgcctc tgacggcctg tcaactcatc 60
acagctgacg actccagacg tacgcagaag catcgccc tgaggcgac caccaaacgc 120
gccacgtcga atcgccccctg caagccgaaa ggacgaaaat gttttccgca tcagaaggac 180
tgctgcaata aaacgtgcac cagatcaaaa tgtccctgat cttccccctt ctgtgctgta 240
tcctttctg cctgagtcct ccttacctga gagtggtcag taaccactca tcaccatctc 300
ctctggagg 309

<210> 130

<211> 72
<212> PRT
<213> Conus ermineus

<400> 130
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg
20 25 30

Ala Leu Arg Ser Thr Thr Lys Arg Ala Thr Ser Asn Arg Pro Cys Lys
35 40 45

Pro Lys Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Asn Lys
50 55 60

Thr Cys Thr Arg Ser Lys Cys Pro
65 70

<210> 131

<211> 27

<212> PRT

<213> Conus ermineus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 1, 4, 11 and 27 is Pro or Hyp

<400> 131

Xaa Xaa Lys Xaa Lys Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys
1 5 10 15

Cys Asn Lys Thr Cys Thr Arg Ser Lys Cys Xaa
20 25

<210> 132

<211> 308

<212> DNA

<213> Conus ermineus

<400> 132

aactcatcac agctgatgac tccagaggtt cgccggacga tcgtgccctg aggtcgacca 60
ccaaactctc catgctgact cggccctgct ggtttccgg aacacccgtt ggtactgata 120
gttttatgctg cgggtggatgc aatgttatcca aaagtaaatg taacttagctg attcggcg 180

tgaacttccc ccttctgtgc tctatccttt tctgcccag tcctccatac ctgagaatgg 240
 tcatgaacca ctcatcacct actcctctgg agacctcaga agagctacac tgaaataaaa 300
 gcgcttgc 308

<210> 133
 <211> 54
 <212> PRT
 <213> Conus ermineus

<400> 133
 Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Asn Asp Arg Ala Leu
 1 5 10 15
 Arg Ser Thr Thr Lys Leu Ser Met Leu Thr Arg Ala Cys Trp Ser Ser
 20 25 30
 Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys Gly Gly Cys Asn Val
 35 40 45
 Ser Lys Ser Lys Cys Asn
 50

<210> 134
 <211> 27
 <212> PRT
 <213> Conus ermineus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at 8 residue is Pro or Hyp; Xaa at residue 3 is
 Trp or Bromo-Trp

<400> 134
 Ala Cys Xaa Ser Ser Gly Thr Xaa Cys Gly Thr Asp Ser Leu Cys Cys
 1 5 10 15
 Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn
 20 25

<210> 135
 <211> 385
 <212> DNA
 <213> Conus geographus

<400> 135
 ggatccatga aactgacgtg cgtggtgatc gtcgccgtgc tgctcctgac ggcctgtcaa 60
 ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgcctggg gtcgaccacc 120
 gaactctcct tgtcgactcg ctgcaagtca cccggatctt catgttcacc gactagttat 180
 aattgctgca ggtcttgcaa tccatacgcc aaaagatgtt acggctaatac cagcgcctga 240
 tcttccccct tctgtgctct atcccttcct gtctgagtcc tccttacctg agagtggtca 300
 tgaaccactc ctcaccaactc tctctggagg cttcggagga gctacattga aataaaagcc 360
 gcattgtaaa aaaaaaaaaaaaa 385

<210> 136
 <211> 73
 <212> PRT

<213> Conus geographus

<400> 136

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ala Leu Gly Ser Thr Thr Glu Leu Ser Leu Ser Thr Arg Cys Lys Ser
35 40 45

Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys
50 55 60

Asn Pro Tyr Ala Lys Arg Cys Tyr Gly
65 70

<210> 137

<211> 27

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at
residue 13, 22 and 27 is Tyr, 125I-Tyr,
mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
or O-phospho-Tyr

<400> 137

Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
1 5 10 15

Arg Ser Cys Asn Xaa Xaa Ala Lys Arg Cys Xaa
20 25

<210> 138

<211> 396

<212> DNA

<213> Conus geographus

<400> 138

ggatccatga aactgacgtg tgtggtgatc gtcgccgtgc tgctcctgac ggcctgtcaa 60

ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgcctgag gtcgtccacc 120

aaactcacct tgtcgactcg ctgcaaatca cccggaactc catgttcaag gggtatgcgt 180

gattgctgca cgccttgctt gttatacagc aacaaatgta ggcgtacta acccagcgcc 240

tgatcttccc cttctgtgc tctattcctt tctgcctgag tcctccttac ctgaaagtgg 300

tcatgaacca ctcatcacct acttctctgg aggcttcaga agagctacat tgaaataaaa 360

gccgcattgc aatgacaaaaa aaaaaaaaaa aaaaaaa 396

<210> 139

<211> 74

<212> PRT

<213> Conus geographus

<400> 139

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Ser Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser
 35 40 45

Pro Gly Thr Pro Cys Ser Arg Gly Met Arg Asp Cys Cys Thr Pro Cys
 50 55 60

Leu Leu Tyr Ser Asn Lys Cys Arg Arg Tyr
 65 70

<210> 140

<211> 29

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(29)

<223> Xaa at residue 4, 7 and 18 is Pro or Hyp; Xaa at residue 22 and 29 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 140

Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys
 1 5 10 15

Thr Xaa Cys Leu Leu Xaa Ser Asn Lys Cys Arg Arg Xaa
 20 25

<210> 141

<211> 407

<212> DNA

<213> Conus geographus

<400> 141

ggaattccgt ttctgcgtcg cttccttgg catcacaaaa accatcatca aaatgaaaact 60

gacgtgtgtg gtgatcgctg ccgtgctgct cctgacggcc tgtcaactca tcacagctga 120

tgactccaga ggtacgcaga agcatcgatgc cctgggtcg accaccgaac tctccttgc 180

gactcgctgc aagtaccccg gatcttcatg ttcaccgact agttataatt gctgcaggta 240

ttgcaatcca tacaccaaaa gatgttacgg ctaatccagc gcctgatctt ccctgctctg 300

agtcctccctt acctgagagt ggtcatgaac cactcatcac ctacttctt aggccgttcg 360

gaggagctac attgaaataa aagccgcatt gaaaaaaaaaaaaaaa 407

<210> 142

<211> 73

<212> PRT

<213> Conus geographus

<400> 142

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Gly Ser Thr Thr Glu Leu Ser Leu Ser Thr Arg Cys Lys Ser
 35 40 45

Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys
 50 55 60

Asn Pro Tyr Thr Lys Arg Cys Tyr Gly
 65 70

<210> 143
<211> 27
<212> PRT
<213> Conus geographus

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at
 residue 13, 22 and 27 is Tyr, 125I-Tyr,
 mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr

<400> 143
Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
 1 5 10 15

Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys Xaa
 20 25

<210> 144
<211> 28
<212> PRT
<213> Conus geographus

<220>
<221> PEPTIDE
<222> (1)..(28)
<223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at
 residue 13, 22 and 27 is Tyr, 125I-Tyr,
 mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr

<400> 144
Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
 1 5 10 15

Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys Xaa Gly
 20 25

<210> 145
<211> 26
<212> PRT
<213> Conus geographus

<220>
<221> PEPTIDE
<222> (1)..(26)
<223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at
 residue 13 and 22 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 145
Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
 1 5 10 15

Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys
20 25

<210> 146

<211> 314

<212> DNA

<213> Conus geographus

<400> 146

catcacagct gatgactcca gaggtacgca gaagcatcggt gccctgaggt cgtccaccaa	60
actcaccttg tcgactcgct gcaaattcacc cggaactcca tggtaaggg gtatgcgtga	120
ttgctgcacg tcttgcttgt tatacagcaa caaatgttagg cgctactaac ccagcgcctg	180
atcttccccc ttctgtgctc tattccttgc tgcctgagtc ctccttacct gaaagtggtc	240
atgaaccact catcacctac ttctctggag gcttcagaag agctacattg aaataaaaagc	300
cgcattgcaa tgac	314

<210> 147

<211> 55

<212> PRT

<213> Conus geographus

<400> 147

Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg Ala Leu Arg	
1 5 10 15	

Ser Ser Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser Pro Gly Thr	
20 25 30	

Pro Cys Ser Arg Gly Met Arg Asp Cys Cys Thr Ser Cys Leu Leu Tyr	
35 40 45	

Ser Asn Lys Cys Arg Arg Tyr	
50 55	

<210> 148

<211> 29

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(29)

<223> Xaa at residue 4 and 7 is Pro or Hyp; Xaa at
residue 22 and 29 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 148

Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys	
1 5 10 15	

Thr Ser Cys Leu Leu Xaa Ser Asn Lys Cys Arg Arg Xaa	
20 25	

<210> 149

<211> 29

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(29)
 <223> Xaa at residue 4 and 7 is Pro or Hyp; Xaa at
 residue 22 and 29 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 149
 Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys
 1 5 10 15

Thr Ser Cys Leu Ser Xaa Ser Asn Lys Cys Arg Arg Xaa	
20 25	

<210> 150
 <211> 380
 <212> DNA
 <213> Conus laterculatus

<400> 150
 accaaaaacca tcatcaaaaat gaaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac cgctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcgacca ccaatctctc catgctgact cggaaagtgct ggccttccgg aagctattgt 180
 cgtgcgaata gttaaatgctg cagtggatgc gatcggaaaca gaaataaatg ttactagctg 240
 attcggcgtc tgaaccttcct cttctgtgc tctatccctt tctgcccag tcctccatac 300
 ctgagagtggtt tcatgaacca ctcaactcct actcctctgg aggccctcaga agagctacat 360
 tggaaataaaaa gcccattgc 380

<210> 151
 <211> 72
 <212> PRT
 <213> Conus laterculatus

<400> 151
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg	
20 25 30	

Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp
 35 40 45

Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys Ser Gly Cys
 50 55 60

Asp Arg Asn Arg Asn Lys Cys Tyr
 65 70

<210> 152
 <211> 27
 <212> PRT
 <213> Conus laterculatus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 4 is Pro or Hyp; Xaa at residue 3
 is Trp or Bromo-Trp; Xaa at residue 8 and 27 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr

<400> 152
Lys Cys Xaa Xaa Ser Gly Ser Xaa Cys Arg Ala Asn Ser Lys Cys Cys
1 5 10 15

Ser Gly Cys Asp Arg Asn Arg Asn Lys Cys Xaa
20 25

<210> 153
<211> 367
<212> DNA
<213> Conus laterculatus

<400> 153
acccaaaacca tcataaaaaat gaaactgacg tgggtggta tcgtcgccgt gctgctcctg 60
acggcctgtc aactcatcac agctgatgac tccagaggta cgccagaagca tcgtgccctg 120
aggtcgacca ccaaactctc catatcgact cgctgccttc ctccggatc atattgtaag 180
gacacaacgg aagtctgctg ctcttcttgc cttcaattcg ctcagatatg ttcgggttga 240
tctccctct tcttgctct atcctttct gcctgagtc tccataacctg agaatggta 300
tgaaccactc aacatctact cctctggagg cctcagaaga gctatattga aataaaagcc 360
gcattgc 367

<210> 154
<211> 73
<212> PRT
<213> Conus laterculatus

<400> 154
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Ile Ser Thr Arg Cys Leu Pro
35 40 45

Pro Gly Ser Tyr Cys Lys Ala Thr Thr Glu Val Cys Cys Ser Ser Cys
50 55 60

Leu Gln Phe Ala Gln Ile Cys Ser Gly
65 70

<210> 155
<211> 27
<212> PRT
<213> Conus laterculatus

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residue 13 is Glu or gamma-carboxy Glu; Xaa
at residue 3 and 4 is Pro or Hyp; Xaa at residue 7
is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
O-sulpho-Tyr or O-phospho-Tyr

<400> 155
Cys Leu Xaa Xaa Gly Ser Xaa Cys Lys Ala Thr Thr Xaa Val Cys Cys
1 5 10 15

Ser Ser Cys Leu Gln Phe Ala Gln Ile Cys Ser
 20 25

<210> 156
 <211> 373
 <212> DNA
 <213> Conus laterculatus

<400> 156
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcaagaagca tcgtgccctg 120
 aggtcgacca ccaatctctc catgtcgact cgctgcaagt ctcccgatc atcatgttagc 180
 gtgtctatgc gtaactgctg cacttcttgc aattcacgca ccaagaaatg tacgcgacgt 240
 ggctgaacctt cccccttctg tgctctatcc ttttctgccc gagtcctcca tacctgagag 300
 tggtcatgaa ccactcaaca tctactcctc tggaggcctc agaagagcta tattgaaata 360
 aaagccgcat tgc 373

<210> 157
 <211> 75
 <212> PRT
 <213> Conus laterculatus

<400> 157
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Ser
 35 40 45

Pro Gly Ser Ser Cys Ser Val Ser Met Arg Asn Cys Cys Thr Ser Cys
 50 55 60

Asn Ser Arg Thr Lys Lys Cys Thr Arg Arg Gly
 65 70 75

<210> 158
 <211> 29
 <212> PRT
 <213> Conus laterculatus

<220>
 <221> PEPTIDE
 <222> (1)..(29)
 <223> Xaa at residue 3 is Pro or Hyp

<400> 158
 Cys Lys Ser Xaa Gly Ser Ser Cys Ser Val Ser Met Arg Asn Cys Cys
 1 5 10 15

Thr Ser Cys Asn Ser Arg Thr Lys Lys Cys Thr Arg Arg
 20 25

<210> 159
 <211> 330
 <212> DNA
 <213> Conus laterculatus

<400> 159
 accaaaacca tcatcaaaat gaaaactgacg tgtgtggta tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcgacaa ccaaactctc catgctgact cgacgtgct ggccttcgg aacagcttgt 180
 ggtattgata gtaactgctg cagtggatgc aatgtatcca gaagtaaatg taactagctg 240
 attcggcgtc taaacttcct cttctgcct gagtcctcca tacctgagag tggcatgaa 300
 ccacatcatc acctcatctc tggaggcctc 330

<210> 160
 <211> 72
 <212> PRT
 <213> Conus laterculatus

<400> 160
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys	Gln	Leu	Ile	Thr	Ala	Asp	Asp	Ser	Arg	Gly	Thr	Gln	Lys	His	Arg
		20				25						30			

Ala	Leu	Arg	Ser	Thr	Thr	Lys	Leu	Ser	Met	Leu	Thr	Arg	Thr	Cys	Trp
		35				40			45						

Pro	Ser	Gly	Thr	Ala	Cys	Gly	Ile	Asp	Ser	Asn	Cys	Cys	Ser	Gly	Cys
	50				55					60					

Asn	Val	Ser	Arg	Ser	Lys	Cys	Asn								
	65				70										

<210> 161
 <211> 27
 <212> PRT
 <213> Conus laterculatus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 4 is Pro or Hyp; Xaa at residue 3
 is Trp or Bromo-Trp

<400> 161
 Thr Cys Xaa Xaa Ser Gly Thr Ala Cys Gly Ile Asp Ser Asn Cys Cys
 1 5 10 15

Ser	Gly	Cys	Asn	Val	Ser	Arg	Ser	Lys	Cys	Asn					
		20				25									

<210> 162
 <211> 363
 <212> DNA
 <213> Conus laterculatus

<400> 162
 accaaaacca tcatcaaaat gaaaactgacg tgtgtggta tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcgacca ccaatctctc catgctgact cgaaatgtgct ggccttcgg aagctattgt 180

cgtgcgaata gtaaatgctg cagtggatgc gatcggaaca gaagtaaatg taactagctg 240
 attcggcgtc taaacctcct ccttctgcct gagtcctcca tacctgagag tggtcatgaa 300
 ccactcatca cctactcctc tggaggcctc aaaggagcta cattgaaata aaagccgcat 360
 tgc 363

<210> 163
 <211> 72
 <212> PRT
 <213> Conus laterculatus

<400> 163
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp
 35 40 45

Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys Ser Gly Cys
 50 55 60

Asp Arg Asn Arg Ser Lys Cys Asn
 65 70

<210> 164
 <211> 27
 <212> PRT
 <213> Conus laterculatus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue4 is Pro or Hyp; Xaa at residue 3 is
 Trp or Bromo-Trp; Xaa at residue 8 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr

<400> 164
 Lys Cys Xaa Xaa Ser Gly Ser Xaa Cys Arg Ala Asn Ser Lys Cys Cys
 1 5 10 15

Ser Gly Cys Asp Arg Asn Arg Ser Lys Cys Asn
 20 25

<210> 165
 <211> 391
 <212> DNA
 <213> Conus leopardus

<220>
 <221> misc_feature
 <222> (1)..(391)
 <223> n may be any nucleotide

<400> 165
 atgaaaactga cgtgtgttgt gatcgtagct gtgctgttcc tgacggcctg tcaactcact 60
 acagctgaca tctccagagg tacgcggaaag cgtcgtgctc tgaggtcgac caccaaactc 120
 tccaggtcgc tctttgagtg cgcgcccttcc ggtggacggtt gtggaaaaaa 180

tgcgaaggat attgcgatgg ggaaagcact tcatgtgtga gtggccata cagcatctga	240
tcttcccccc ttcaagtgcct tatccttttc tgccctgagtc ctccataacct ctgagcggtc	300
atgaaccact caacacctac tcctctggag gcttcaggga actatattaa aataaagccg	360
cattgcaacg aaanaaaaaa aaaaaaaaaa a	391

<210> 166
<211> 79
<212> PRT
<213> Conus leopardus

<400> 166			
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala			
1	5	10	15
Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Arg Lys Arg Arg			
20	25	30	
Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Ser Leu Phe Glu Cys Ala			
35	40	45	
Pro Ser Gly Gly Arg Cys Gly Phe Leu Lys Ser Cys Cys Glu Gly Tyr			
50	55	60	
Cys Asp Gly Glu Ser Thr Ser Cys Val Ser Gly Pro Tyr Ser Ile			
65	70	75	

<210> 167
<211> 37
<212> PRT
<213> Conus leopardus

<220>			
<221> PEPTIDE			
<222> (1)..(37)			
<223> Xaa at residue 4, 20 and 26 is Glu or gamma-carboxy			
Glu; Xaa at residue 7 and 34 is Pro or Hyp; Xaa at			
residue 22 and 35 is Tyr, 125I-Tyr, mono-iodo-Tyr,			
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr			
<400> 167			
Ser Leu Phe Xaa Cys Ala Xaa Ser Gly Gly Arg Cys Gly Phe Leu Lys			
1	5	10	15
Ser Cys Cys Xaa Gly Xaa Cys Asp Gly Xaa Ser Thr Ser Cys Val Ser			
20	25	30	
Gly Xaa Xaa Ser Ile			
35			

<210> 168
<211> 365
<212> DNA
<213> Conus leopardus

<400> 168	
atgaaaactga cgtgtgttgt gatcgctcgct gtgctgttcc tgacggcctg tcaactcact	60
acagctgaca tctccagagg tacgtgaaag catcggttg tggggtcgac cacccggactc	120
tccccgtggc ccttggactg cacggctccc agtcaacctt gtggttatcc tccttaggtgc	180

tgtggacatt gcgatgtacg cagggtatgt acgagtggt gatccggcgt ctgatcttc 240
 cgccttctgt gctgtatcct tttctgcctg agtcctccat acccgtgagt ggtcatgaac 300
 cactcaacac ctactcctct ggaggctca gaggaactat attaaaataa agccgcattg 360
 caatg 365

<210> 169
<211> 73
<212> PRT
<213> Conus leopardus

<400> 169
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Trp Lys His Arg
 20 25 30

Gly Val Gly Ser Thr Thr Gly Leu Ser Pro Trp Pro Leu Asp Cys Thr
 35 40 45

Ala Pro Ser Gln Pro Cys Gly Tyr Phe Pro Arg Cys Cys Gly His Cys
 50 55 60

Asp Val Arg Arg Val Cys Thr Ser Gly
 65 70

<210> 170
<211> 30
<212> PRT
<213> Conus leopardus

<220>
<221> PEPTIDE
<222> (1)..(30)
<223> Xaa at residue 2, 8, 11 and 16 is Pro or Hyp; Xaa
 at residue 1 is Trp or Bromo-Trp; Xaa at residue 14
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 170
 Xaa Xaa Leu Asp Cys Thr Ala Xaa Ser Gln Xaa Cys Gly Xaa Phe Xaa
 1 5 10 15

Arg Cys Cys Gly His Cys Asp Val Arg Arg Val Cys Thr Ser
 20 25 30

<210> 171
<211> 381
<212> DNA
<213> Conus leopardus

<400> 171
 atgaaaactga cgtgtgttgt gatcgctcgct gtgtgttcc tgacggcctg tcaactcact 60
 acagctgaca tctccagagg tacgcggaaag catcgctgctc tgaggtcgac caccaaactc 120
 tccaggtcgc cctctaggta catgtctccc ggtggaaattt gtgggtgattt tggtgactgc 180
 tgcgaaattt gcaatgtgtta cggtatgt gtgagtgact taccggcat ctgatcttc 240
 cgccttctgt gctctatcct tttctgcctg agtcctccat acccctgagt ggtcatggac 300

cactcaacac ctactcctct ggaggcttca gaggaactac attaaaataa agccgcattg 360
 caaaaaaaaaa aaaaaaaaaa a 381

<210> 172
<211> 77
<212> PRT
<213> Conus leopardus

<400> 172
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Arg Lys His Arg
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Ser Pro Ser Arg Cys Met
 35 40 45

Ser Pro Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Glu Ile Cys
 50 55 60

Asn Val Tyr Gly Ile Cys Val Ser Asp Leu Pro Gly Ile
 65 70 75

<210> 173
<211> 31
<212> PRT
<213> Conus leopardus

<220>
<221> PEPTIDE
<222> (1)..(31)
<223> Xaa at residue 16 is Glu or gamma-carboxy Glu; Xaa
 at residue 4 and 29 is Pro or Hyp; Xaa at residue
 21 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 173
 Cys Met Ser Xaa Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Xaa
 1 5 10 15

Ile Cys Asn Val Xaa Gly Ile Cys Val Ser Asp Leu Xaa Gly Ile
 20 25 30

<210> 174
<211> 404
<212> DNA
<213> Conus leopardus

<400> 174
 atgaaaactga cgtgtgtgg gatcgtcgct gtgctgttcc tgacggcctg tcaactcact 60
 acagctgatg attccagagg tacacggaag catcgtgctc tgaggtcaac caccaaactc 120
 tccaggtggc ccaggtactg cgccgcctccc ggtggagctt gtgggtttt tgatcactgc 180
 tgcggatatt gcgaaacgtt ttacaatacg tgttagatgag ttggctgatc cggcgcttga 240
 tctttccgcc ttctgttgct ctatctttt ctgcctgagt cctccatcac cccgttgagt 300
 ggtccatgaa ccactccaac acctactccc tccttggaaag cttccaaagg aaacgacatt 360
 taaaataaat tccccattgc aattggaaaa aaaaaaaaaa aaaa 404

<210> 175
 <211> 72
 <212> PRT
 <213> Conus leopardus

<400> 175
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Thr Thr Ala Asp Asp Ser Arg Gly Thr Arg Lys His Arg
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Trp Pro Arg Tyr Cys Ala
 35 40 45

Pro Pro Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys Gly Tyr Cys
 50 55 60

Glu Thr Phe Tyr Asn Thr Cys Arg
 65 70

<210> 176
 <211> 27
 <212> PRT
 <213> Conus leopardus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 20 is Glu or gamma-carboxy Glu; Xaa
 at residue 4 and 5 is Pro or Hyp; Xaa at residue 1,
 18 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 176
 Xaa Cys Ala Xaa Xaa Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys
 1 5 10 15

Gly Xaa Cys Xaa Thr Phe Xaa Asn Thr Cys Arg
 20 25

<210> 177
 <211> 292
 <212> DNA
 <213> Conus lynceus

<400> 177
 atgaaaactga cgtgtgtggatgcgtcgcc gtgctgctcc tgacggcctgtcaactcatc 60
 acagctgatg actccagacg tacacagaag catcggtcccc tgagggtcgac caccaatctc 120
 tccatgtcga ctcgctgcaa gtctcccgaa tcaccatgta gtgtgacatc gtataactgc 180
 tgcactttt gctcttcata cactaagaaa tgtcgggcct ctatgtAAC cactcatcac 240
 ctactcctct ggaggcctca gaagagctac actgaaataa aagccgcatt gg 292

<210> 178
 <211> 75
 <212> PRT
 <213> Conus lynceus

<400> 178
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Ser
 35 40 45

Pro Gly Ser Pro Cys Ser Val Thr Ser Tyr Asn Cys Cys Thr Phe Cys
 50 55 60

Ser Ser Tyr Thr Lys Lys Cys Arg Ala Ser Leu
 65 70 75

<210> 179

<211> 30

<212> PRT

<213> Conus lynceus

<220>

<221> PEPTIDE

<222> (1)..(30)

<223> Xaa at residue 4 and 7 is Pro or Hyp; Xaa at
 residue 13 and 22 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 179

Cys Lys Ser Xaa Gly Ser Xaa Cys Ser Val Thr Ser Xaa Asn Cys Cys
 1 5 10 15

Thr Phe Cys Ser Ser Xaa Thr Lys Lys Cys Arg Ala Ser Leu
 20 25 30

<210> 180

<211> 355

<212> DNA

<213> Conus lynceus

<400> 180

atgaaaactga cgtgtgtgg gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc 60

acagctgatg actccagagg tacgcagaag catcgtgccc tgaggtcgac caccaaacta 120

tccatgtata ctcgctgcgc aggtccagga gcaatttgc ctaatagggt atgctgcggt 180

tattgcagta aaagaacaca tctatgtcat tcgcgaactg gctgatcttc cccttctgt 240

gctctatcct ttttctgcct gagtcctcca tacctgagaa tggtcatgaa ccactcatca 300

cctactcctc ttggagacct cagaggagct acactgaaat aaaagccgca ttggc 355

<210> 181

<211> 74

<212> PRT

<213> Conus lynceus

<400> 181

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Tyr Thr Arg Cys Ala Gly
 35 40 45

Pro Gly Ala Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr Cys Ser Lys
 50 55 60

Arg Thr His Leu Cys His Ser Arg Thr Gly
 65 70

<210> 182
<211> 28
<212> PRT
<213> Conus lynceus

<220>
<221> PEPTIDE
<222> (1)..(28)
<223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at
 residue 16 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
<400> 182

Cys Ala Gly Xaa Gly Ala Ile Cys Xaa Asn Arg Val Cys Cys Gly Xaa
 1 5 10 15

Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr
 20 25

<210> 183
<211> 361
<212> DNA
<213> Conus lynceus

<400> 183
atgaaaactga cgtgtgtgg gatcgctgcc gtgctgctgc tagcggcctg tcaactacta 60
cacgctgatg actccagagg tacgcagaag actgctgccc gaggtcgacc accaaaaactc 120
tccatgctga ctcgggcctg ctggcttcc ggaacacacctt gtggtaactga tagtttatgc 180
tgcggtgat gcaatgtatc caaaagtaaa tgtaacttagc tgattcggcg tctgaacttc 240
ccccttctgt gctctatcct tttctgccc agtcctccat acctgagaat ggtcatgaac 300
cactcatcac ctactcctct ggagacctca gaagagctac actgaaataa aagcgcattg 360
c 361

<210> 184
<211> 72
<212> PRT
<213> Conus lynceus

<400> 184
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Ala Ala
1 5 10 15

Cys Gln Leu Leu His Ala Asp Asp Ser Arg Gly Thr Gln Lys Thr Ala
 20 25 30

Ala Arg Gly Arg Pro Pro Lys Leu Ser Met Leu Thr Arg Ala Cys Trp
 35 40 45

Ser Ser Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys Gly Gly Cys
 50 55 60

Asn Val Ser Lys Ser Lys Cys Asn
 65 70

<210> 185

<211> 27

<212> PRT

<213> Conus lynceus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 8 is Pro or Hyp; Xaa at residue 3
is Trp or Bromo-Trp

<400> 185

Ala Cys Xaa Ser Ser Gly Thr Xaa Cys Gly Thr Asp Ser Leu Cys Cys
1 5 10 15 /Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn
20 25

<210> 186

<211> 364

<212> DNA

<213> Conus lynceus

<400> 186

atgaaaactga cgtgtgtgg gatcggtcgcc gagctactcc taacggcctg tcaactcatc 60
acagctgatg actccagagg tacgcagaag catcggtccc tgagggtcgac caccaatctc 120
tccatgctga ctgcgaagtgc ctggtctccc ggaacctatt gtcgtgcgc tagtaaatgc 180
tgccgtggat gcgatcagaa cagaaataaa tgttactagc tgattcggcg tctgaacttc 240
ctccttctgt gctctatcct ttttctgcct gagtcctcca tacctgagaa tggtcatgaa 300
ccactcatca cctactcctc tggaggcctc agaggagcct acactgaaat aaaagccgca 360
ttgg 364

<210> 187

<211> 72

<212> PRT

<213> Conus lynceus

<400> 187

Met Lys Leu Thr Cys Val Val Ile Val Ala Glu Leu Leu Leu Thr Ala
1 5 10 15Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp
35 40 45Ser Pro Gly Thr Tyr Cys Arg Ala His Ser Lys Cys Cys Arg Gly Cys
50 55 60Asp Gln Asn Arg Asn Lys Cys Tyr
65 70

<210> 188

<211> 27

<212> PRT

<213> Conus lynceus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 5 is Pro or Hyp; Xaa at residue 3
 is Trp or Bromo-Trp; Xaa at residue 8 and 27 is
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 188
 Lys Cys Xaa Ser Xaa Gly Thr Xaa Cys Arg Ala His Ser Lys Cys Cys
 1 5 10 15

Arg Gly Cys Asp Gln Asn Arg Asn Lys Cys Xaa
 20 25

<210> 189
 <211> 318
 <212> DNA
 <213> Conus magus

<400> 189
 accaaaaacca tcatcaaaat gaaaactgacg tttgtggta tcgtcgccgt gctgctccctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcggaca ccaaactctc catgtcgact cgctgcaagg gtacagggaa accatgcagt 180
 aggattgcgt ataactgctg caccggttct tgcagatcag gtaaatgtgg ctgatccagt 240
 gcctgatctt cccccttctg tgctctatcc tttttctgcc tgagtcctcc ttacctgaga 300
 gtggcatga accactca 318

<210> 190
 <211> 71
 <212> PRT
 <213> Conus magus

<400> 190
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 . 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
 . 35 40 45

Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser
 . 50 55 60

Cys Arg Ser Gly Lys Cys Gly
 . 65 70

<210> 191
 <211> 25
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 191
 Cys Lys Gly Thr Gly Lys Xaa Cys Ser Arg Ile Ala Xaa Asn Cys Cys
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 192
 <211> 259
 <212> DNA
 <213> Conus magus

<400> 192
 accaaaaacca tcatcaaaat gaaaactgacg tgggtggta tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgccagaagca tcgtgccctg 120
 aagtccggaca ccaaactctc catgttaact ttgcgctgctg catcttacgg aaaaccttgt 180
 ggtatttaca acgactgctg caatacatgc gatccagcca gaaagacatg tacgttagctg 240
 atccggcgtc tgatcttcc 259

<210> 193
 <211> 72
 <212> PRT
 <213> Conus magus

<400> 193
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Lys Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
 35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Thr Cys
 50 55 60

Asp Pro Ala Arg Lys Thr Cys Thr
 65 70

<210> 194
 <211> 26
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at
 residue 4 and 11 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 194
 Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn
 1 5 10 15

Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr
 20 25

<210> 195

<211> 254
 <212> DNA
 <213> Conus magus

<400> 195
 gaattttcag catcaccaaa accatcatca aaatgaaaact gacgtgtgtg gtgatcg 60
 ccgtgctgct cctgacggcc tgtcaactca tcacagctga tgactccaga ggtacgcaga 120
 agcatcgatgc cctgaggctg gacaccaaacc tctccatgtc aactcgctgc aagggtaaag 180
 gagcatcatg tcataaggact tcgttatgact gctgcaccgg ttcttgcaac agaggtaaat 240
 ttggctgatc cgcc 254

<210> 196
 <211> 71
 <212> PRT
 <213> Conus magus

<400> 196
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
 35 40 45

Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser
 50 55 60

Cys Asn Arg Gly Lys Phe Gly
 65 70

<210> 197
 <211> 25
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 197
 Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Xaa Asp Cys Cys
 1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Lys Cys
 20 25

<210> 198
 <211> 358
 <212> DNA
 <213> Conus miles

<400> 198
 ggatccatga aactgacgtg cgtggtgatc atcgccatgc tgttcctgac agcctatcaa 60
 ctcgctacag ctgcgagcta cgccaaaggt aaacagaagc atcgtgtct gaggccagct 120
 gacaaacacc tcaggttgc acagcgttgc aatgatcgcg gtggaggttg cagtcaacat 180

cctcaactgct gcgggtggAAC ttgcaataag cttattggcg tatgtctgta aagctggtct 240
 gccgtctgat attccctttc tgtgcttcAT cctctttgc ctgagtcATc catacctgtg 300
 aatggtaAG agccactcaa tacctattcc tctggggcT tcagaggaac tactttac 358

<210> 199
<211> 74
<212> PRT
<213> Conus miles

<400> 199
Met Lys Leu Thr Cys Val Val Ile Ile Ala Met Leu Phe Leu Thr Ala
1 5 10 15

Tyr Gln Leu Ala Thr Ala Ala Ser Tyr Ala Lys Gly Lys Gln Lys His
20 25 30

Arg Ala Leu Arg Pro Ala Asp Lys His Leu Arg Leu Thr Lys Arg Cys
35 40 45

Asn Asp Arg Gly Gly Cys Ser Gln His Pro His Cys Cys Gly Gly
50 55 60

Thr Cys Asn Lys Leu Ile Gly Val Cys Leu
65 70

<210> 200
<211> 27
<212> PRT
<213> Conus arenatus

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residue 12 is Pro or Hyp

<400> 200
Cys Asn Asp Arg Gly Gly Cys Ser Gln His Xaa His Cys Cys Gly
1 5 10 15

Gly Thr Cys Asn Lys Leu Ile Gly Val Cys Leu
20 25

<210> 201
<211> 292
<212> DNA
<213> Conus monachus

<400> 201
acccaaaaccca tcataaaaaat gaaaactgacg agtgtggta tcgtcgccgt gctgctccctg 60
acggcctgtc aactcatcac agctgatgac tccagaggta cgccagaagca tcgtgccctg 120
aggtcggaca cccaaactctc catatcgact cgctgcaagt ctacaggaaa atcatgcagt 180
aggattgcgt ataactgctg caccggttct tgcaGATcag gtAAATgtgg ctgatccagc 240
gcctgatctt ccccccttctg tgctctatcc ttttctgcct gagtcctcct ta 292

<210> 202
<211> 71
<212> PRT
<213> Conus monachus

<400> 202
 Met Lys Leu Thr Ser Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Ile Ser Thr Arg Cys Lys Ser
 35 40 45

Thr Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser
 50 55 60

Cys Arg Ser Gly Lys Cys Gly
 65 70

<210> 203

<211> 25

<212> PRT

<213> Conus monachus

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 203

Cys Lys Ser Thr Gly Lys Ser Cys Ser Arg Ile Ala Xaa Asn Cys Cys
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 204

<211> 258

<212> DNA

<213> Conus monachus

<400> 204

accaaaaacca tcatcaaaat gaaaactgacg agtgtggta tcgtcgccgt gctgctcctg 60

acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120

aggtcggaca ccaacctctc catgtcgact cgctgcaagg gtaaaggatc ttcatgtagt 180

aggaccatgt ataactgctg caccggttct tgcaacagag gtaaatgtgg ctgatccagc 240

gcctgatctt ccccccttc 258

<210> 205

<211> 71

<212> PRT

<213> Conus monachus

<400> 205

Met Lys Leu Thr Ser Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Asp Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Gly
 35 40 45

Lys Gly Ser Ser Cys Ser Arg Thr Met Tyr Asn Cys Cys Thr Gly Ser
 50 55 60

Cys Asn Arg Gly Lys Cys Gly
 65 70

<210> 206
 <211> 25
 <212> PRT
 <213> Conus monachus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 206
 Cys Lys Gly Lys Gly Ser Ser Cys Ser Arg Thr Met Xaa Asn Cys Cys
 1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Lys Cys
 20 25

<210> 207
 <211> 258
 <212> DNA
 <213> Conus obscurus

<400> 207
 ctctctctct ctctgctgga caggtcgccct ccctgcataa aaggcggatc gtcataccgc 60
 ggtactacgg gagtctgttg cggttttgc agtgatttcg gctataaatg tagggactat 120
 ccccaaaaact gatcttcccc ctttgtgct ctatcctttt ctgtccgagt cctcctgacc 180
 tgagagtgg catgaaccac tcatacaccta cccctctggg gcttcacagg atctacattg 240
 aaataaaaagc cgcatggc 258

<210> 208
 <211> 39
 <212> PRT
 <213> Conus obscurus

<400> 208
 Leu Leu Asp Arg Ser Pro Pro Cys Met Lys Gly Gly Ser Ser Cys Arg
 1 5 10 15

Gly Thr Thr Gly Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Tyr Lys
 20 25 30

Cys Arg Asp Tyr Pro Gln Asn
 35

<210> 209
 <211> 35
 <212> PRT
 <213> Conus obscurus

<220>
 <221> PEPTIDE
 <222> (1)..(35)
 <223> Xaa at residue 2, 3 and 33 is Pro or Hyp; Xaa at

residue 27 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 209
Ser Xaa Xaa Cys Met Lys Gly Gly Ser Ser Cys Arg Gly Thr Thr Gly
1 5 10 15

Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Xaa Lys Cys Arg Asp Xaa
20 25 30
Xaa Gln Asn
35

<210> 210

<211> 259

<212> DNA

<213> Conus obscurus

<400> 210

ctctctctct ctctgctgga caggtcgact cgctgcttgc ctgacggaac gtcttgccctt 60

ttagtagga tcagatgctg cggtaattgc agttcaatct taaagtcatg tgtgagctga 120

tccagcgggtt gatcttcctc cctctgtgct ccattctttt ctgcctgagt tctccttacc 180

tgagagtggc catgaaccac tcatcaccta ctcttctgga ggcttcagag gagctacatt 240

gaaataaaaag ccgcattgc 259

<210> 211

<211> 32

<212> PRT

<213> Conus obscurus

<400> 211

Arg Ser Thr Arg Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg
1 5 10 15

Ile Arg Cys Cys Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
20 25 30

<210> 212

<211> 28

<212> PRT

<213> Conus monachus

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residue 3 is Pro or Hyp

<400> 212

Cys Leu Xaa Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
1 5 10 15

Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
20 25

<210> 213

<211> 330

<212> DNA

<213> Conus pulicarius

<220>

<221> misc_feature

<222> (1)..(330)

<223> n may be any nucleotide

<400> 213
atgaaactga cgtgtgtgg t gatcatcgcc gtgctgttcc tgacggcctg tcaactcatt 60
acagctgaga cttaactccag aggtaagcag a a g c a c c g t g cttttaggtc aactgacaaa 120
aactccaagt tgacttaggc a gtgctcgcc a acggtgat cttgttctcg tcattttcac 180
tgctgcagcc tctattgaa taaaatact ggcgtatgt a ttgcaaccta ataccctgt 240
gtggtcatga accactcaat accctctcct ctggaggctt cagaggaact gcattgaaat 300
aaaactgcat tgcnttgacc aaaaaaaaaaaaa 330

<210> 214

<211> 76

<212> PRT

<213> Conus pulicarius

<400> 214

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Lys His
20 25 30

Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys
35 40 45

Ser Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys Ser Leu
50 55 60

Tyr Cys Asn Lys Asn Thr Gly Val Cys Ile Ala Thr
65 70 75

<210> 215

<211> 30

<212> PRT

<213> Conus pulicarius

<220>

<221> PEPTIDE

<222> (1)..(30)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue
4 is Pro or Hyp; Xaa at residue 19 is Tyr, 125I-Tyr,
mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
O-phospho-Tyr

<400> 215

Xaa Cys Ser Xaa Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys
1 5 10 15

Ser Leu Xaa Cys Asn Lys Asn Thr Gly Val Cys Ile Ala Thr
20 25 30

<210> 216

<211> 282

<212> DNA

<213> Conus purpurascens

<400> 216

atgaaactga cgtgtgtgg t gatcgatcgcc gtgctgttcc tgacggcctg tcaactcatt 60

acagctgatg actccagacg tacgcagaag catcgatccc tgaggatcgac caccaaaggc 120

gccacgtcga atcgcccctg caagacaccc ggacgaaaat gtttccgca tcagaaggac 180
 tgctgcggtc gagcgtgcat catcacaata tgtccctgat cttccccctt ctgtgctgta 240
 tcctttctg cctgagtctc cttacctgag agtggcatg aa 282

<210> 217
 <211> 72
 <212> PRT
 <213> Conus purpurascens

<400> 217
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Gly Ala Thr Ser Asn Arg Pro Cys Lys
 35 40 45

Thr Pro Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Gly Arg
 50 55 60

Ala Cys Ile Ile Thr Ile Cys Pro
 65 70

<210> 218
 <211> 27
 <212> PRT
 <213> Conus purpurascens

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 1, 5, 11 and 27 is Pro or Hyp

<400> 218
 Xaa Cys Lys Thr Xaa Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys
 1 5 10 15

Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Xaa
 20 25

<210> 219
 <211> 340
 <212> DNA
 <213> Conus purpurascens

<400> 219
 accaaaaacca tcatcaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcaagaagca tcgtgccctg 120
 aggtcgacca ccaaactctt cacgtcgaaa agctgcaagc ttcccccggagc atattgtaat 180
 gcagaagatt atgactgctg ccttagatgc aaagttggag gtacatgtgg ctgatccagt 240
 gcctgatctt cccccctctg tgctctatcc ttttctgcct gagtcctcct tacctaagag 300
 tggtcatgaa ccactcatca ccttctcctc tggaggcttc 340

<210> 220
 <211> 71
 <212> PRT

<213> Conus purpurascens

<400> 220

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala	
1	5
	10
	15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg	
20	25
	30

Ala Leu Arg Ser Thr Thr Lys Leu Phe Thr Ser Lys Ser Cys Lys Leu	
35	40
	45

Pro Gly Ala Tyr Cys Asn Ala Glu Asp Tyr Asp Cys Cys Leu Arg Cys	
50	55
	60

Lys Val Gly Gly Thr Cys Gly	
65	70

<210> 221

<211> 26

<212> PRT

<213> Conus purpurascens

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 12 is Glu or gamma-carboxy Glu; Xaa at residue 5 is Pro or Hyp; Xaa at residue 8 and 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 221

Ser Cys Lys Leu Xaa Gly Ala Xaa Cys Asn Ala Xaa Asp Xaa Asp Cys	
1	5
	10
	15

Cys Leu Arg Cys Lys Val Gly Gly Thr Cys	
20	25

<210> 222

<211> 317

<212> DNA

<213> Conus purpurascens

<400> 222

atgaaaactga cgtgtgtggatgcgtcgcc gtgctgttcc tgacggcctg tcaactcatc	60
--	----

acagctgatg actccagacg tacgcagaag catcggtccc tgaggctgac caccaaacgc	120
---	-----

gccacgtcga atcgccccctg caagaaaaacc ggacgaaaat gttttccgca tcagaaggac	180
---	-----

tgctgcggtc gagcgtgcat catcacaata tgtccctgat cttccccctt ctgtgctgta	240
---	-----

tcctttctg cctgagtcct ccttacctga gagtggtcat gaaccactca tcaccccttc	300
--	-----

ctctggagggc ttcaagag	317
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<210> 223

<211> 72

<212> PRT

<213> Conus purpurascens

<400> 223

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala	
1	5
	10
	15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Arg Ala Thr Ser Asn Arg Pro Cys Lys
 35 40 45
 Lys Thr Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Gly Arg
 50 55 60

Ala Cys Ile Ile Thr Ile Cys Pro
 65 70

<210> 224

<211> 27

<212> PRT

<213> Conus purpurascens

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 1, 11 and 27 is Pro or Hyp

<400> 224

Xaa Cys Lys Lys Thr Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys
 1 5 10 15

Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Xaa
 20 25

<210> 225

<211> 328

<212> DNA

<213> Conus radiatus

<400> 225

gctgatgcct gatcttcatc gttctccct gtctcctttg gcatcaccaa aaccatcatc 60

aaaatgaaac tgacgtgtgt ggtgatcgta gccgtgctgg tcctgacggc ctgtcaactc 120

atcacagctg atgactccag aggtatgcag aaacatcatg ccctgggtc gatcagcagt 180

ctctttaagt cgaccgtca tggctgaaa cccctcaaac gtcgttgaaa caatgataaa 240

gaatgctgca gcaaattttg caattcagtc cgaaaggagt gtggataaat ggctaaaaaa 300

ctgaataaaa gccgcattgc aaaaaaaaaa 328

<210> 226

<211> 74

<212> PRT

<213> Conus radiatus

<400> 226

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Val Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Met Gln Lys His His
 20 25 30

Ala Leu Gly Ser Ile Ser Ser Leu Phe Lys Ser Thr Arg His Gly Cys
 35 40 45

Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys Cys Ser Lys
 50 55 60

Phe Cys Asn Ser Val Arg Lys Gln Cys Gly
 65 70

<210> 227
<211> 28
<212> PRT
<213> Conus radiatus

<220>
<221> PEPTIDE
<222> (1)..(28)
<223> Xaa at residue 15 is Glu or gamma-carboxy Glu;
Xaa at residue 5 is Pro or Hyp

<400> 227
His Gly Cys Lys Xaa Leu Lys Arg Arg Cys Phe Asn Asp Lys Xaa Cys
1 5 10 15

Cys Ser Lys Phe Cys Asn Ser Val Arg Lys Gln Cys
20 25

<210> 228
<211> 250
<212> DNA
<213> Conus radiatus

<400> 228
gaaatgaaac tgacgtgtgt ggtgatcgtc gccgtgctgg tcctgacggc ctgtcaactc 60
atcacagctg atgactccag aggtatgcag aaacatcatg ccctgggtc gatcagcagt 120
ctctttaagt cgaccgctcg tggctgcaaa cccctcaaac gtcgttgaaa caatgataaa 180
gaatgctgca gcaaattttg caattcagtc cggaaaccagg gtggataaaat ggctaaaaac 240
tgaataaaaag 250

<210> 229
<211> 74
<212> PRT
<213> Conus radiatus

<400> 229
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Val Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Met Gln Lys His His
20 25 30

Ala Leu Gly Ser Ile Ser Ser Leu Phe Lys Ser Thr Arg Arg Gly Cys
35 40 45

Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys Cys Ser Lys
50 55 60

Phe Cys Asn Ser Val Arg Asn Gln Cys Gly
65 70

<210> 230
<211> 28
<212> PRT
<213> Conus radiatus

<220>
<221> PEPTIDE

<222> (1)..(28)
 <223> Xaa at residue 15 is Glu or gamma-carboxy Glu;
 Xaa at residue 5 is Pro or Hyp

<400> 230
 Arg Gly Cys Lys Xaa Leu Lys Arg Arg Cys Phe Asn Asp Lys Xaa Cys
 1 5 10 15

Cys Ser Lys Phe Cys Asn Ser Val Arg Asn Gln Cys
 20 25

<210> 231
 <211> 435
 <212> DNA
 <213> Conus radiatus

<400> 231
 ggaattccgc ttgcacggcg aacctgactt catctttctt ccctgcctcc tttggcatca 60
 ccaaaaaccat catcaaaaatg aaactgacgt gtgtggtgat cgtcgccgtg ctggtcctga 120
 cggcctgtca actcatcaca gctgatgact ccagaggtat gcagaagcat catgccctga 180
 ggtcgatcac caaactctcc ctgtcgactc gctgcaaacc tcccggatca ccatgttagag 240
 tttcttcgta taactgctgc tcttcttgca aatcatacaa caagaaatgt ggctgaacct 300
 ccccttctgt gctctatcct tttcctgccc gagtcctcca tacctgagag tagtcatgaa 360
 ccactgatta cctactcctc tggagggcct cagaggagct actttgaaat aaaagccgc 420
 attgcaaaaa aaaaaa 435

<210> 232
 <211> 72
 <212> PRT
 <213> Conus radiatus

<400> 232
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Val Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Met Gln Lys His His
 20 25 30

Ala Leu Arg Ser Ile Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Pro
 35 40 45

Pro Gly Ser Pro Cys Arg Val Ser Ser Tyr Asn Cys Cys Ser Ser Cys
 50 55 60

Lys Ser Tyr Asn Lys Lys Cys Gly
 65 70

<210> 233
 <211> 27
 <212> PRT
 <213> Conus radiatus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 3, 4 and 7 is Pro or Hyp; Xaa at
 residue 13 and 22 is Tyr, 125I-Tyr, mono-iodo-Tyr,

di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 233
 Cys Lys Xaa Xaa Gly Ser Xaa Cys Arg Val Ser Ser Xaa Asn Cys Cys
 1 5 10 15

Ser Ser Cys Lys Ser Xaa Asn Lys Lys Cys Gly
 20 25

<210> 234
 <211> 392
 <212> DNA
 <213> Conus rattus

<400> 234
 ggatccatga aactgacgtg catggtgatc atcgccgtgc tggccctgac agcctgtcaa 60
 ttcgatacag ctgcgagcta cgacaaaggta aagcagaaac ctcctactct gaggccagct 120
 gacaaacaca tcaggttgc acagcgttgc aatgctcgca atgatggttg cagtcaacat 180
 tctcaatgct gcagtggatc ttgcaataag actgcaggcg tatgtctgta aagctggct 240
 gccgtctgat attccctttc tggctttat cctctttgc ctgagtcattc catacctgtg 300
 aatggtaag agccactcaa tacctactcc tctggggct tcagaggaac tacattaaat 360
 aaagccacat tgcaaaaaaaaaaaaaaa aa 392

<210> 235
 <211> 74
 <212> PRT
 <213> Conus rattus

<400> 235
 Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Phe Asp Thr Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro
 20 25 30

Pro Thr Leu Arg Pro Ala Asp Lys His Ile Arg Leu Thr Lys Arg Cys
 35 40 45

Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser Gly
 50 55 60

Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
 65 70

<210> 236
 <211> 27
 <212> PRT
 <213> Conus rattus

<400> 236
 Cys Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser
 1 5 10 15

Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
 20 25

<210> 237
 <211> 395

<212> DNA
 <213> Conus rattus
 <400> 237
 ggatccatga aactgacgtg cgtggtgatc atcgccgtgc tggccctgac agcctgtcaa 60
 ctgcgtgcag ctgcgagcta cgacaaaggt aagcagaaac ctcctactct gaggccagct 120
 gacaaaacact tcaggttcat caagcgttgc aatgctcgca atagtggttg cagtcacat 180
 cctcaatgct gcagtggatc ttgcaataag actgcaggcg tatgtctgta aagctggct 240
 gccgtctgtat attccctttc tgtgctttat cctctttgc ctgagtcatc catacctgtg 300
 aatggttaag agccactcaa tacctactcc tctggggct tcagaggaac tacattaaat 360
 aaagccacat tgcaacgaaa aaaaaaaaaa aaaaa 395

 <210> 238
 <211> 74
 <212> PRT
 <213> Conus rattus

 <400> 238
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

 Cys Gln Leu Asp Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro
 20 25 30

 Pro Thr Leu Arg Pro Ala Asp Lys His Phe Arg Leu Ile Lys Arg Cys
 35 40 45

 Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser Gly
 50 55 60

 Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
 65 70

 <210> 239
 <211> 27
 <212> PRT
 <213> Conus rattus

 <220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 12 is Pro or Hyp

 <400> 239
 Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Xaa Gln Cys Cys Ser
 1 5 10 15

 Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
 20 25

 <210> 240
 <211> 390
 <212> DNA
 <213> Conus rattus

 <400> 240
 ggatccatga aactgacgtg tgggtgatc atcgccgtgc tggccctgac agcctgtcaa 60
 ttcgatacag ctgcgagcta cgacaaaggt aagcagaaac ctcctactct gaggccagct 120

gacaaacact tcaggttgc caagcgttgc aatgctcgca atagtggttg cagtcacat 180
 cctcaatgct gcagtgatc ttgcaataag actttggcg tatgtctgta aagctggct 240

 gccgtctgat attccctttc tgtgcttat cctctttgc ctgagtcattc catacctgtg 300

 aatggtaag agccactcaa tacctactcc tctggggct tcagaggaac tacattaaat 360

 aaagccacat tgaaaaaaaaaaaaaaaaaaaaaaa 390

 <210> 241
 <211> 74
 <212> PRT
 <213> Conus rattus

 <400> 241
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

 Cys Gln Phe Asp Thr Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro
 20 25 30

 Pro Thr Leu Arg Pro Ala Asp Lys His Phe Arg Leu Ile Lys Arg Cys
 35 40 45

 Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser Gly
 50 55 60

 Ser Cys Asn Lys Thr Leu Gly Val Cys Leu
 65 70

 <210> 242
 <211> 27
 <212> PRT
 <213> Conus rattus

 <220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 12 is Pro or Hyp

 <400> 242
 Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Xaa Gln Cys Cys Ser
 1 5 10 15

 Gly Ser Cys Asn Lys Thr Leu Gly Val Cys Leu
 20 25

 <210> 243
 <211> 379
 <212> DNA
 <213> Conus stercusmuscarum

 <400> 243
 accaaaaacca tcatcaaat gaaactgacg tgggtgtca tcgtcgccgt gctgctcctg 60

 acggcctgtc aactcatcac agctgatgac tccagaggta cgccagaagca tcgtgccctg 120

 aggtcgaaga ccaaactctc catgtcgact cgctgcaaga gtaaaggagc aaaatgttca 180

 aggcttatgt atgactgctg cagcggttct tgcagcggct acacaggtag atgtggctga 240

 tccagcgcct gatctcccc cttctgtgct ctatcctttt ctgcctgggt ctccttacc 300

 tgagagtgtt catgaaccac tcatcaccta ctcccttgaa ggcctcagag gagttacaat 360

gaaataaaag ccgcattgc	379
<210> 244	
<211> 73	
<212> PRT	
<213> Conus stercusmuscarum	
<400> 244	
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala	
1 5 10 15	
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg	
20 25 30	
Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ser	
35 40 45	
Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys Ser Gly Ser	
50 55 60	
Cys Ser Gly Tyr Thr Gly Arg Cys Gly	
65 70	
<210> 245	
<211> 27	
<212> PRT	
<213> Conus stercusmuscarum	
<220>	
<221> PEPTIDE	
<222> (1)..(27)	
<223> Xaa at residue 13 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr	
<400> 245	
Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Xaa Asp Cys Cys	
1 5 10 15	
Ser Gly Ser Cys Ser Gly Xaa Thr Gly Arg Cys	
20 25	
<210> 246	
<211> 35	
<212> PRT	
<213> Conus stercusmuscarum	
<220>	
<221> PEPTIDE	
<222> (1)..(35)	
<223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21, 24 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr	
<400> 246	
Thr Thr Ser Cys Met Gln Ala Gly Ser Xaa Cys Gly Ser Thr Thr Arg	
1 5 10 15	
Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa	
20 25 30	
Xaa Ser Asn	
35	
<210> 247	

<211> 380
 <212> DNA
 <213> Conus stercusmuscarum

<400> 247
 accaaaacca tcatcaaaat gaaactgacg tgtgtggta tcgtcgccgt gctgctcctg 60
 acgacacctgc aactcatcac agctgatgac tccagaggta cgccaggagca tcgtgccctg 120
 aggtcgaaga ccaaactctc catgttaact ttgcgctgctg catcttacgg aaaaccttgt 180
 ggtattgaca acgactgctg caatgcatgc gatccagcca gaaatatatg tacgttagctg 240
 atccggcgtc tgatcttccc cttctgtgc tctatcctt tctgcctgag tcctccttac 300
 ctgagagtgg tcatgaacca ctcatcatct actctcctgg aggccctcaga ggagctacaa 360
 tgaaataaaa gccgcattgc 380

<210> 248
 <211> 72
 <212> PRT
 <213> Conus stercusmuscarum

<400> 248
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
 20 25 30

Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
 35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Ala Cys
 50 55 60

Asp Pro Ala Arg Asn Ile Cys Thr
 65 70

<210> 249
 <211> 26
 <212> PRT
 <213> Conus stercusmuscarum

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at
 residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 249
 Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn
 1 5 10 15

Ala Cys Asp Xaa Ala Arg Asn Ile Cys Thr
 20 25

<210> 250
 <211> 388
 <212> DNA
 <213> Conus stercusmuscarum
 <400> 250
 ggatccatga aactgacgtg tgtggtgatt gtcgcccgtgc tgctcctgac ggcctgtcaa 60

ctcatcacag ctgatgactc cagaggtacg caggagcatc gtgccctgag gtcgaagacc 120
 aaactctcca tgttaacttt gcgcgtcgta tcttacggaa aaccttgtgg tattgacaac 180
 gactgctgca atgcatgcga tccagccaga aatatatgta cgtagctgat ccggcgtctg 240
 atcttcccccc ttctgtgctc tatccttttc tgccctggtc ctccttacct gagagtggc 300
 atgaaccact catcacctac tcctctggag gcctcagagg agttacaatg aaataaaaagc 360
 cgcattgcaa aaaaaaaaaa aaaaaaaaa 388

 <210> 251
 <211> 72
 <212> PRT
 <213> Conus stercusmuscarum

 <400> 251
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
 20 25 30

 Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Val
 35 40 45

 Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Ala Cys
 50 55 60

 Asp Pro Ala Arg Asn Ile Cys Thr
 65 70

 <210> 252
 <211> 26
 <212> PRT
 <213> Conus stercusmuscarum

 <220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at
 residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

 <400> 252
 Cys Val Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn
 1 5 10 15

 Ala Cys Asp Xaa Ala Arg Asn Ile Cys Thr
 20 25

 <210> 253
 <211> 264
 <212> DNA
 <213> Conus striatus

 <400> 253
 accaaaaacca tcatcaaaat gaaactgacg tgtgtggta tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgccagaagca tcgttccctg
 aggtcgacca ccaaagtctc caaggcgact gactgcattg aagccggaaa ttattgcgga 120
 180
 cctactgtta tgaaaatctg ctgcggctt tgcagtcac acagcaaaat atgtatgaac 240

tatcccaaaa attgatcttc cccc 264

<210> 254
<211> 78
<212> PRT
<213> Conus striatus

<400> 254
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ala Thr Asp Cys Ile Glu
35 40 45

Ala Gly Asn Tyr Cys Gly Pro Thr Val Met Lys Ile Cys Cys Gly Phe
50 55 60

Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn Tyr Pro Lys Asn
65 70 75

<210> 255
<211> 36
<212> PRT
<213> Conus striatus

<220>
<221> PEPTIDE
<222> (1)..(36)
<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at
residue 13, 25 and 34 is Pro or Hyp; Xaa at residue
10, 26 and 33 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 255
Ala Thr Asp Cys Ile Xaa Ala Gly Asn Xaa Cys Gly Xaa Thr Val Met
1 5 10 15

Lys Ile Cys Cys Gly Phe Cys Ser Xaa Xaa Ser Lys Ile Cys Met Asn
20 25 30

Xaa Xaa Lys Asn
35

<210> 256
<211> 233
<212> DNA
<213> Conus striatus

<400> 256
gtcgactcgc tgcaagctta aaggacaatc atgtcgtagg actatgtatg actgctgcag 60
cggttcttgc ggcaggagag gtaaatgtgg ctgatccagc gcctgatctc cccccttctg 120
tgctctatcc ttttctgcct gggtcctcct tacctgagag tggtcatgaa ccactcatca 180
cctactcctc tggaggcctc agaggagcta caatgaaata aaagccgcat tgc 233

<210> 257
<211> 30
<212> PRT
<213> Conus striatus

<400> 257
 Ser Thr Arg Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Tyr
 1 5 10 15
 Asp Cys Cys Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys Gly
 20 25 30
 <210> 258
 <211> 26
 <212> PRT
 <213> Conus striatus
 <220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
 <400> 258
 Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Xaa Asp Cys Cys
 1 5 10 15
 Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys
 20 25
 <210> 259
 <211> 310
 <212> DNA
 <213> Conus striatus
 <400> 259
 accaaaaacca tcatcaaaat gaaaactgacg tgggtggta tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcggaca ccaaactctc catgtcgact cgctgcaagg ctgcaggaaa atcatgcagt 180
 aggattgcgt ataactgctg caccggttct tgcatcgatcg gtaaatgcgg ctgatccagc 240
 gcctgatctt ccccccttctg tgctctatcc tttctgcctg agtcctctta cctgagagt 300
 gtcatgaacc 310
 <210> 260
 <211> 71
 <212> PRT
 <213> Conus striatus
 <400> 260
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ala
 35 40 45
 Ala Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser
 50 55 60
 Cys Arg Ser Gly Lys Cys Gly
 65 70

<210> 261
 <211> 25
 <212> PRT
 <213> Conus striatus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 261
 Cys Lys Ala Ala Gly Lys Ser Cys Ser Arg Ile Ala Xaa Asn Cys Cys
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 262
 <211> 256
 <212> DNA
 <213> Conus striatus

<400> 262
 accaaaaacca tcatcaaaat gaaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg 120
 aggtcggaca ccaaactctc catgttaact ttgcgctgca aatcttacgg aaaaccttgt 180
 ggtattttaca acgactgctg caatgcatgc gatccagcca aaaagacatg tacgttagctg 240
 atccggcgtc tgatct 256

<210> 263
 <211> 72
 <212> PRT
 <213> Conus striatus

<400> 263
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Glu
 35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Ala Cys
 50 55 60

Asp Pro Ala Lys Lys Thr Cys Thr
 65 70

<210> 264
 <211> 26
 <212> PRT
 <213> Conus striatus

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 2 is Glu or gamma-carboxy Glu; Xaa

at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 and 11 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 264

Cys	Xaa	Ser	Xaa	Gly	Lys	Xaa	Cys	Gly	Ile	Xaa	Asn	Asp	Cys	Cys	Asn
1				5					10				15		

Ala	Cys	Asp	Xaa	Ala	Lys	Lys	Thr	Cys	Thr
			20				25		

<210> 265

<211> 229

<212> DNA

<213> Conus striatus

<400> 265

tctaggcctt	ccggcagccc	ctgtgggttt	actagtata	gctgtggtag	atgcataagg	60
------------	------------	------------	-----------	------------	------------	----

ggtaaatgt	cgtagctcat	cggcgctctg	atcttcccc	ttcttgctc	catcctttc	120
-----------	------------	------------	-----------	-----------	-----------	-----

tgccctgagtc	ctccttacct	gagagtggtc	gtgaaccact	catcgctac	tcctctggag	180
-------------	------------	------------	------------	-----------	------------	-----

gcttcagagg	ggctacacta	aaataaaaagc	tatattgcaa	tgaaaaaaaa	229
------------	------------	-------------	------------	------------	-----

<210> 266

<211> 24

<212> PRT

<213> Conus striatus

<400> 266

Cys	Arg	Ser	Ser	Gly	Ser	Pro	Cys	Gly	Val	Thr	Ser	Ile	Cys	Cys	Gly
1				5					10				15		

Arg	Cys	Tyr	Arg	Gly	Lys	Cys	Thr
		20					

<210> 267

<211> 24

<212> PRT

<213> Conus striatus

<220>

<221> PEPTIDE

<222> (1)..(24)

<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 19 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 267

Cys	Arg	Ser	Ser	Gly	Ser	Xaa	Cys	Gly	Val	Thr	Ser	Ile	Cys	Cys	Gly
1				5					10				15		

Arg	Cys	Xaa	Arg	Gly	Lys	Cys	Thr
		20					

<210> 268

<211> 26

<212> PRT

<213> Conus striatus

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,

di-iodo-Tyr, O -sulpho-Tyr or O-phospho-Tyr

<400> 268

Cys	Lys	Leu	Lys	Gly	Gln	Ser	Cys	Arg	Lys	Thr	Ser	Xaa	Asp	Cys	Cys
1				5				10					15		

Ser	Gly	Ser	Cys	Gly	Arg	Ser	Gly	Lys	Cys
		20				25			

<210> 269

<211> 292

<212> DNA

<213> Conus striolatus

<400> 269

acccaaaacca	tcatcaaaat	gaaactgacg	tgtgtggta	tcgtcgctt	gctgctcctg	60
-------------	------------	------------	-----------	-----------	------------	----

acgacctgtc	gtctcatcac	agctgatgac	tccagaggta	cgcagaagca	tcgttccctg	120
------------	------------	------------	------------	------------	------------	-----

aggtcgacta	ctaaagtctc	catgtcgact	cgctgcaagg	gtaaaggagc	atcatgtctt	180
------------	------------	------------	------------	------------	------------	-----

aggactgcgt	atgactgctg	caccggttct	tgcaacagag	gtagatgtgg	ctgatccagc	240
------------	------------	------------	------------	------------	------------	-----

gtctgatctt	cccccttctg	tgctctatcc	ttttctgctt	gagtcctcct	ta	292
------------	------------	------------	------------	------------	----	-----

<210> 270

<211> 71

<212> PRT

<213> Conus striolatus

<400> 270

Met	Lys	Leu	Thr	Cys	Val	Val	Ile	Val	Val	Leu	Leu	Leu	Leu	Thr	Thr
1				5				10					15		

Cys	Arg	Leu	Ile	Thr	Ala	Asp	Asp	Ser	Arg	Gly	Thr	Gln	Lys	His	Arg
		20				25			30						

Ser	Leu	Arg	Ser	Thr	Thr	Lys	Val	Ser	Met	Ser	Thr	Arg	Cys	Lys	Gly
		35			40						45				

Lys	Gly	Ala	Ser	Cys	Leu	Arg	Thr	Ala	Tyr	Asp	Cys	Cys	Thr	Gly	Ser
		50			55			60							

Cys	Asn	Arg	Gly	Arg	Cys	Gly
65				70		

<210> 271

<211> 25

<212> PRT

<213> Conus striolatus

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 271

Cys	Lys	Gly	Lys	Gly	Ala	Ser	Cys	Leu	Arg	Thr	Ala	Xaa	Asp	Cys	Cys
1				5				10					15		

Thr	Gly	Ser	Cys	Asn	Arg	Gly	Arg	Cys
		20			25			

<210> 272

<211> 259

<212> DNA

<213> Conus striolatus

<400> 272

acccaaaacca	tcatcaaaat	gaaactgacg	tgtgtggtga	tcgtcgccgt	tctgctgacg	60
gcgtgtcaac	tcatcacagc	tgaggactcc	agaggtacac	agaagcatcg	taccctgagg	120
tcgaccgtca	gacgctccaa	gtccgagttg	actacgagat	gcaggccttc	aggatccaac	180
tgtggtaata	ttagtatctg	ctgtggtaga	tgcgttaaca	gaagatgtac	gtagctcatc	240
ggcggtctga	tcttcccc					259

<210> 273

<211> 71

<212> PRT

<213> Conus striolatus

<400> 273

Met	Lys	Leu	Thr	Cys	Val	Val	Ile	Val	Ala	Val	Leu	Leu	Thr	Ala	Cys
1					5					10				15	

Gln	Leu	Ile	Thr	Ala	Glu	Asp	Ser	Arg	Gly	Thr	Gln	Lys	His	Arg	Thr
							20			25			30		

Leu	Arg	Ser	Thr	Val	Arg	Arg	Ser	Lys	Ser	Glu	Leu	Thr	Thr	Arg	Cys
						35		40				45			

Arg	Pro	Ser	Gly	Ser	Asn	Cys	Gly	Asn	Ile	Ser	Ile	Cys	Cys	Gly	Arg
					50			55			60				

Cys	Val	Asn	Arg	Arg	Cys	Thr
					65	70

<210> 274

<211> 24

<212> PRT

<213> Conus striolatus

<220>

<221> PEPTIDE

<222> (1)..(24)

<223> Xaa at residue 3 is Pro or Hyp

<400> 274

Cys	Arg	Xaa	Ser	Gly	Ser	Asn	Cys	Gly	Asn	Ile	Ser	Ile	Cys	Cys	Gly
1					5				10			15			

Arg	Cys	Val	Asn	Arg	Arg	Cys	Thr
					20		

<210> 275

<211> 280

<212> DNA

<213> Conus striolatus

<400> 275

acccaaaacca	tcatcaaaat	gaaactgacg	tgtgtggtga	tcgtcgccgt	tctgttcctg	60
-------------	------------	------------	------------	------------	------------	----

acggcgtgtc	aactcatcac	agctgaggac	tccagaggtt	cacagaagca	tcgttccctg	120
------------	------------	------------	------------	------------	------------	-----

aggtcgacta	ccaaagtctc	caagtcgact	agctgcatga	aagccgggtc	ttattgcgtc	180
------------	------------	------------	------------	------------	------------	-----

gctactacga gaatctgctg cggttattgc gcttatttcg gcaaaatatg tattgactat 240
 cccaaaaact gatcttcccc ctactgtgct ctatcctttt 280

<210> 276
 <211> 77
 <212> PRT
 <213> Conus striolatus

<400> 276
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys
 35 40 45

Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg Ile Cys Cys Gly Tyr Cys
 50 55 60

Ala Tyr Phe Gly Lys Ile Cys Ile Asp Tyr Pro Lys Asn
 65 70 75

<210> 277
 <211> 35
 <212> PRT
 <213> Conus striolatus

<220>
 <221> PEPTIDE
 <222> (1)..(35)
 <223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10,
 21, 24 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 277
 Ser Thr Ser Cys Met Lys Ala Gly Ser Xaa Cys Val Ala Thr Thr Arg
 1 5 10 15

Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Ile Cys Ile Asp Xaa
 20 25 30

Xaa Lys Asn
 35

<210> 278
 <211> 174
 <212> DNA
 <213> Conus textile

<400> 278
 gttgactcggtactgcacgc ctcatggagg acattgtgg tatcataatg actgctgcag 60
 tcatcaatgc aatataaaca gaaataaatg tgtagtagctg atctggcattc tgatctgtgc 120

tcgtccttac ctgagagtgg tcatgaacca ctcatcacct actcctctgg aggc 174

<210> 279
 <211> 31
 <212> PRT
 <213> Conus textile

<400> 279

Leu Thr Arg Tyr Cys Thr Pro His Gly Gly His Cys Gly Tyr His Asn
 1 5 10 15

Asp Cys Cys Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu
 20 25 30

<210> 280
<211> 28
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(28)
<223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa
 at residue 4 is Pro or Hyp; Xaa at residue 1 and 11
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 280
Xaa Cys Thr Xaa His Gly Gly His Cys Gly Xaa His Asn Asp Cys Cys
 1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Xaa
 20 25

<210> 281
<211> 28
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(28)
<223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa
 at residue 4 is Pro or Hyp; Xaa at residue 1 and 11
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Tyr

<400> 281
Xaa Cys Thr Xaa Xaa Gly Gly His Cys Gly Xaa His Asn Asp Cys Cys
 1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Xaa
 20 25

<210> 282
<211> 379
<212> DNA
<213> Conus tulipa

<400> 282
acccaaaaccca tcataaaaaat gaaaactgacg tgggtggta tcgtcgccgt gctgctcctg 60
acggcctgtc agctcatcac agctctgcac tccagaggta cgcagaagca tcgtgccctg 120
gggcggacca ccaaactcac cttgtcgact cgctgcaaatt cacccggatc tccatgttca 180
ccgacttagtt ataattgctg ctggtcttgc agtccataca gaaaaaaaaatg taggggctaa 240
tccagcgcct gatttcccc cttctgtgct ctattccttt ctgcctgagt ctccttacc 300
tgaaaagtggt catgaaccac tcatacaccta cttctctgga ggcttcggag gagctacatt 360
gaaataaaaag ccgcattgc 379

<210> 283

<211> 73

<212> PRT

<213> Conus tulipa

<400> 283

Met	Lys	Leu	Thr	Cys	Val	Val	Ile	Val	Ala	Val	Leu	Leu	Leu	Thr	Ala
1					5				10					15	

Cys	Gln	Leu	Ile	Thr	Ala	Leu	His	Ser	Arg	Gly	Thr	Gln	Lys	His	Arg
					20			25				30			

Ala	Leu	Gly	Arg	Thr	Thr	Lys	Leu	Thr	Leu	Ser	Thr	Arg	Cys	Lys	Ser
					35			40				45			

Pro	Gly	Ser	Pro	Cys	Ser	Pro	Thr	Ser	Tyr	Asn	Cys	Cys	Trp	Ser	Cys
					50			55			60				

Ser	Pro	Tyr	Arg	Lys	Lys	Cys	Arg	Gly
				65		70		

<210> 284

<211> 27

<212> PRT

<213> Conus tulipa

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 3, 7, 10 and 21 is Pro or Hyp; Xaa at residue 17 is Trp or Bromo Trp; Xaa at residue 13 and 22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 284

Cys	Lys	Ser	Xaa	Gly	Ser	Xaa	Cys	Ser	Xaa	Thr	Ser	Xaa	Asn	Cys	Cys
1					5				10			15			

Xaa	Ser	Cys	Ser	Xaa	Xaa	Arg	Lys	Lys	Cys	Arg
				20				25		

<210> 285

<211> 379

<212> DNA

<213> Conus tulipa

<400> 285

acccaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60

acggcctgtc agctcatcac agctctgcac tccagaggta cgccagaagca tcgtgccctg 120

gggtcgacca ccaaactcac ctgtcgact cgctgcttgt cacccggatc ttcatgttca 180
ccgacttagtt ataattgctg caggcttgc aatccataca gcagaaaatg taggggctaa 240

tccagcgcct gatcttcccc cttctgtgct ctattcctt ctgcctgagt ctccttacc 300

tgaaagtggc catgaaccac tcatcaccta cttctctgga ggcttcggag gagctacatt 360

gaaataaaag ccgcattgc 379

<210> 286

<211> 73

<212> PRT

<213> Conus tulipa

<400> 286
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Leu His Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Gly Ser Thr Thr Lys Leu Thr Leu Ser Thr Arg Cys Leu Ser
 35 40 45

Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys
 50 55 60

Asn Pro Tyr Ser Arg Lys Cys Arg Gly
 65 70

<210> 287

<211> 27

<212> PRT

<213> Conus tulipa

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at
 residue 13 and 22 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 287

Cys Leu Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
 1 5 10 15

Arg Ser Cys Asn Xaa Xaa Ser Arg Lys Cys Arg
 20 25

<210> 288

<211> 401

<212> DNA

<213> Conus viola

<400> 288

accaaaaacca tcataaaaaat gaaaactgacg tgggtggta tcgtcgccgt gctgctcctg 60

acggcctgtc agtcattac agctgatgac tccagaggta cgcagttgca tcgtgccctg 120

aggaaggcca ccaaactccc cgtgtcgact cgctgcatta cttaggaac acgatgtaa 180

gttccgagtc aatgctgcag atcttcttgc aagaacggtc gttgtgctcc atccccctgaa 240

gaatggtaaa tgtggctgat ccagcgctg atcttcccccc ttctgactgt ctccgacctt 300

ttctgcctga gtcctcctta cctgagaggt gtcataacc actcatcacc tactcccctg 360

gaagcttcag aggagctaca ttgaaataaaa agccgcattt c 401

<210> 289

<211> 76

<212> PRT

<213> Conus viola

<400> 289

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Leu His Arg
 20 25 30

Ala Leu Arg Lys Ala Thr Lys Leu Pro Val Ser Thr Arg Cys Ile Thr
 35 40 45

Leu Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg Ser Ser Cys
 50 55 60

Lys Asn Gly Arg Cys Ala Pro Ser Pro Glu Glu Trp
 65 70 75

<210> 290

<211> 31

<212> PRT

<213> Conus viola

<220>

<221> PEPTIDE

<222> (1)..(31)

<223> Xaa at residue 29 and 30 is Glu or gamma-carboxy
 Glu; Xaa at residue 11, 26 and 28 is Pro or Hyp;
 Xaa at residue 31 is Trp or Bromo-Trp

<400> 290

Cys Ile Thr Leu Gly Thr Arg Cys Lys Val Xaa Ser Gln Cys Cys Arg
 1 5 10 15

Ser Ser Cys Lys Asn Gly Arg Cys Ala Xaa Ser Xaa Xaa Xaa Xaa
 20 25 30

<210> 291

<211> 372

<212> DNA

<213> Conus viola

<400> 291

acccaaaacca tcatcaaaat gaaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60

acggcctgtc agctcattat agctggggac tccagaggta cgcaaggcgc tcgtgccctg 120

aggaaggcca ccaaactctc cgtgtcgact cgctgcaaga gtagaggatc atcatgtcgt 180

aggacttcgt atgactgctg cacgggttct tgcaaaaaatg gttaaatgtgg ctgatccagc 240

gcctgatctt cccccttctg tgctccatcc ttttctgcct gagtcctcct tacctgagag 300

tgggcatgaa ccactcatca cctactccct ggaagcttca gaggagctac attgaaataa 360

aagccgcatt gc 372

<210> 292

<211> 71

<212> PRT

<213> Conus viola

<400> 292

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Ile Ala Gly Asp Ser Arg Gly Thr Gln Leu His Arg
 20 25 30

Ala Leu Arg Lys Ala Thr Lys Leu Ser Val Ser Thr Arg Cys Lys Ser
 35 40 45

Arg Gly Ser Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser
 50 55 60

Cys Arg Asn Gly Lys Cys Gly
 65 70

<210> 293

<211> 25

<212> PRT

<213> Conus viola

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 293

Cys Lys Ser Arg Gly Ser Ser Cys Arg Arg Thr Ser Xaa Asp Cys Cys
 1 5 10 15

Thr Gly Ser Cys Arg Asn Gly Lys Cys
 20 25

<210> 294

<211> 380

<212> DNA

<213> Conus viola

<400> 294

accaaaaacca tcatcaaaaat gaaactgacg tgtgtggcga tcgtcgccgt gctgctcctg 60

acggcctgtc agtcattac agctgaagac tccagaggta cgcatgagca tcttgccctg 120

aagtgcacct ccaaagtctc caagtcgact agctgcattgg aagccagatc ttattgcgga 180

cctgctacta cggaaatctg ctgcgatttt tgcaagtccat tcagcgatag atgtatgaac 240

aatcccaaca attgatcttc ccctttgtgt gctccatctt ttctgcctga gtcctcctta 300

cctgagagtg gtcatgaacc actcatcacc tactcctctg gaggcttcag aggagttaca 360

ttgaaataaa agccgcattgc 380

<210> 295

<211> 78

<212> PRT

<213> Conus viola

<400> 295

Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu
 20 25 30

Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Glu
 35 40 45

Ala Arg Ser Tyr Cys Gly Pro Ala Thr Thr Lys Ile Cys Cys Asp Phe
 50 55 60

Cys Ser Pro Phe Ser Asp Arg Cys Met Asn Asn Pro Asn Asn
 65 70 75

<210> 296
 <211> 36
 <212> PRT
 <213> Conus viola

<220>
 <221> PEPTIDE
 <222> (1)..(36)
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13, 25 and 34 is Pro or Hyp; Xaa at residue 10 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 296
 Ser Thr Ser Cys Met Xaa Ala Arg Ser Xaa Cys Gly Xaa Ala Thr Thr
 1 5 10 15

Lys Ile Cys Cys Asp Phe Cys Ser Xaa Phe Ser Asp Arg Cys Met Asn
 20 25 30

Asn Xaa Asn Asn
 35

<210> 297
 <211> 373
 <212> DNA
 <213> Conus viola

<400> 297
 accaaaacca tcatcaaaat gaaaactgacg tgtgtggta tcgtcgccgt gctgctcctg 60
 acggcctgtc agctcattac agctgaggac tccagaggta cgcagttgca tcgtgccctg 120
 aggaagacca ccaaactctc cttgtcgact cgctgcaagg gtccaggagc catatgtata 180
 aggattgcgt ataactgctg caagtattct tgcggaaatg gtaaatgtgg ctgatccagc 240
 gcctgatctt cccccctgtg tgctccatcc ttttctgcc tgagtcctcc ttacctgaga 300
 gtggcatga accactcatc acctactcct ctggaggctt cagaggagct acattgaaat 360
 aaaagccgca tgc 373

<210> 298
 <211> 71
 <212> PRT
 <213> Conus viola

<400> 298
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg
 20 25 30

Ala Leu Arg Lys Thr Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Gly
 35 40 45

Pro Gly Ala Ile Cys Ile Arg Ile Ala Tyr Asn Cys Cys Lys Tyr Ser
 50 55 60

Cys Gly Asn Gly Lys Cys Gly
 65. 70

<210> 299
 <211> 25
 <212> PRT
 <213> Conus viola

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 3 is Pro or Hyp; Xaa at residue
 13 and 18 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 299
 Cys Lys Gly Xaa Gly Ala Ile Cys Ile Arg Ile Ala Xaa Asn Cys Cys
 1 5 10 15

Lys Xaa Ser Cys Gly Asn Gly Lys Cys
 20 25

<210> 300
 <211> 353
 <212> DNA
 <213> Conus viola

<400> 300
 accaaaaacca tcatcaaaat gaaaactgacg tgggtggtga tcgtcgccgt gctgttcctg 60
 acggcctgtc aattcatcac agctgatgac tccagaagta cgcaagaagca tcgtgccctg
 aggtcgcacca ccaaacactt tatgttgact tggtaactgca cgccttatgg aggacattgt 120
 gtttattata atgactgctg cagtcatcaa tgcaatataa acagaaataa atgtgagtag 180
 ctgatccggc atctgatctg tgctcgccct aacctgagag tggtcatgaa ccactcatca 240
 tctactcctc tggaggcttc agaggagcta catggaaata aaagccgcat tgc 300
 353

<210> 301
 <211> 73
 <212> PRT
 <213> Conus viola

<400> 301
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Phe Ile Thr Ala Asp Asp Ser Arg Ser Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Thr Thr Lys His Phe Met Leu Thr Trp Tyr Cys Thr
 35 40 45

Pro Tyr Gly Gly His Cys Gly Tyr Tyr Asn Asp Cys Cys Ser His Gln
 50 55 60

Cys Asn Ile Asn Arg Asn Lys Cys Glu
 65 70

<210> 302
 <211> 28
 <212> PRT
 <213> Conus viola

<220>
 <221> PEPTIDE
 <222> (1)..(28)

<223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa at residue 4 is Pro or Hyp; Xaa at residue 1, 5, 11 and 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 302

Xaa	Cys	Thr	Xaa	Xaa	Gly	Gly	His	Cys	Gly	Xaa	Xaa	Asn	Asp	Cys	Cys
1				5					10					15	
Ser	His	Gln	Cys	Asn	Ile	Asn	Arg	Asn	Lys	Cys	Xaa				
			20					25							

<210> 303

<211> 294

<212> DNA

<213> Conus pulicarius

<400> 303

ggatccatga	aactgacgtg	cgtggtgatt	atcgccgtgc	tgttcctgac	ggcctgtcaa	60
ctcattacag	ctgagactta	ctccagaggt	aagcagatgc	accgtgctct	gaggtaact	120
gacaaaaact	ccaagttgac	caggaaatgc	acacaccttgc	atggagcttg	tggtttacct	180
acacactgct	gcgggttttg	cgatatggca	aacaacagat	gtctgtaaag	cgtctgata	240
tccccttctg	tgctctatcc	tctttggcct	gagtcatcca	tacctgtgct	cgag	294

<210> 304

<211> 73

<212> PRT

<213> Conus pulicarius

<400> 304

Met	Lys	Leu	Thr	Cys	Val	Val	Ile	Ile	Ala	Val	Leu	Phe	Leu	Thr	Ala
1					5				10				15		

Cys	Gln	Leu	Ile	Thr	Ala	Glu	Thr	Tyr	Ser	Arg	Gly	Lys	Gln	Met	His
				20				25				30			

Arg	Ala	Leu	Arg	Ser	Thr	Asp	Lys	Asn	Ser	Lys	Leu	Thr	Arg	Glu	Cys
				35				40				45			

Thr	Pro	Pro	Asp	Gly	Ala	Cys	Gly	Leu	Pro	Thr	His	Cys	Cys	Gly	Phe
		50				55			60						

Cys	Asp	Met	Ala	Asn	Asn	Arg	Cys	Leu							
		65				70									

<210> 305

<211> 27

<212> PRT

<213> Conus pulicarius

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa at residue 4, 5 and 12 is Pro or Hyp

<400> 305

Xaa	Cys	Thr	Xaa	Xaa	Asp	Gly	Ala	Cys	Gly	Leu	Xaa	Thr	His	Cys	Cys
1				5					10				15		

Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu
 20 25

<210> 306

<211> 294

<212> DNA

<213> Conus pulicarius

<400> 306

ggatccatga aactgacgtg cgtggtgatt atcgccgtgc tgttcctgac ggcctgtcaa 60
 ctcattacag ctgagactta ctccagaggt aagcagatgc accgtgctct gaggtcaact 120
 gacaaaaact cccagttgac cagggaatgc acacacctccag gtggagcttgg tggtttacct 180
 acacactgct gcggggttttgc cgatatggca aacaacagat gtctgtaaag cgtctgatata 240
 tccccttctg tgctctatcc tctttggcct gagtcatcca tacctgtgct cgag 294

<210> 307

<211> 73

<212> PRT

<213> Conus pulicarius

<400> 307

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Met His
 20 25 30

Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Gln Leu Thr Arg Glu Cys
 35 40 45

Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys Gly Phe
 50 55 60

Cys Asp Met Ala Asn Asn Arg Cys Leu
 65 70

<210> 308

<211> 27

<212> PRT

<213> Conus pulicarius

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa
 at residue 4, 5 and 12 is Pro or Hyp

<400> 308

Xaa Cys Thr Xaa Xaa Gly Gly Ala Cys Gly Leu Xaa Thr His Cys Cys
 1 5 10 15

Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu
 20 25

<210> 309

<211> 307

<212> DNA

<213> Conus rattus

<400> 309

ggatccatga aactgacgtg tgtggtgatc atcgccgtgc tgttcctggc agcctgtcaa 60

cctgttacaa ctgagacttt ctccagaggt aaggagaagc gtcgtgctct gaggtcaact 120
 gacggcaact cccggttgac cagggcatgc acgcctgaag gtggagcctg tagtagtggg 180
 cgtcactgct gcggctttg cgataacgtg tcccacacgt gctatggtga aacaccatct 240
 ctccactgat gtttccccctt ctgtgctcta tcttcttttg cctgagtcat ccataccgt 300
 gctcgag 307

<210> 310
<211> 80
<212> PRT
<213> Conus rattus

<400> 310
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Ala Ala
1 5 10 15

Cys Gln Pro Val Thr Thr Glu Thr Phe Ser Arg Gly Lys Glu Lys Arg
20 25 30

Arg Ala Leu Arg Ser Thr Asp Gly Asn Ser Arg Leu Thr Arg Ala Cys
35 40 45

Thr Pro Glu Gly Gly Ala Cys Ser Ser Gly Arg His Cys Cys Gly Phe
50 55 60

Cys Asp Asn Val Ser His Thr Cys Tyr Gly Glu Thr Pro Ser Leu His
65 70 75 80

<210> 311
<211> 34
<212> PRT
<213> Conus rattus

<220>
<221> PEPTIDE
<222> (1)..(34)
<223> Xaa at residue 5 and 29 is Glu or gamma-carboxy
Glu; Xaa at residue 4 and 31 is Pro or Hyp; Xaa at
residue 27 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 311
Ala Cys Thr Xaa Xaa Gly Gly Ala Cys Ser Ser Gly Arg His Cys Cys
1 5 10 15

Gly Phe Cys Asp Asn Val Ser His Thr Cys Xaa Gly Xaa Thr Xaa Ser
20 25 30

Leu His

<210> 312
<211> 342
<212> DNA
<213> Conus stercusmuscarum

<220>
<221> misc_feature
<222> (1)..(342)
<223> n may be any nucleotide

<400> 312

agatccatga aactgacgtg cgtggtgatc gtcgccgtgc tgctcctgac ggctgtcaa 60
 ctcatcacag ctgatgactc cagaggtacg caggagcatc gtgcctgag gtcggacacc 120
 aaactccccca tatcgactcg ctgcaagggt aaaggagcat catgtcataa gactatgtat 180
 gactgctgca gcggttcctg caccagaggt agatgtggct gatccagcgc ctgatcttcc 240
 cccttctgtg ctctatcctt ttctgcctga gtcatcatac ctgtgctcga gcgttactag 300
 tggatccgag ctcggatcca agcttggcgt aatcataaaa nc 342

<210> 313

<211> 71

<212> PRT

<213> Conus stercusmuscarum

<400> 313

Met	Lys	Leu	Thr	Cys	Val	Val	Ile	Val	Ala	Val	Leu	Leu	Leu	Thr	Ala
1				5					10					15	

Cys	Gln	Leu	Ile	Thr	Ala	Asp	Asp	Ser	Arg	Gly	Thr	Gln	Glu	His	Arg
				20				25				30			

Ala	Leu	Arg	Ser	Asp	Thr	Lys	Leu	Pro	Ile	Ser	Thr	Arg	Cys	Lys	Gly
		35				40					45				

Lys	Gly	Ala	Ser	Cys	His	Lys	Thr	Met	Tyr	Asp	Cys	Cys	Ser	Gly	Ser
50					55					60					

Cys	Thr	Arg	Gly	Arg	Cys	Gly
65				70		

<210> 314

<211> 25

<212> PRT

<213> Conus stercusmuscarum

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 314

Cys	Lys	Gly	Lys	Gly	Ala	Ser	Cys	His	Lys	Thr	Met	Xaa	Asp	Cys	Cys
1					5				10				15		

Ser	Gly	Ser	Cys	Thr	Arg	Gly	Arg	Cys
			20				25	

<210> 315

<211> 33

<212> PRT

<213> Conus arenatus

<400> 315

Gln	Cys	Ser	Ala	Asn	Gly	Gly	Ser	Cys	Thr	Arg	His	Phe	His	Cys	Cys
1					5				10				15		

Ser	Leu	Tyr	Cys	Asn	Lys	Asp	Ser	Ser	Val	Cys	Val	Ala	Thr	Ser	Tyr
				20				25				30			

Pro

<210> 316

<211> 28

<212> PRT

<213> Conus arenatus

<400> 316

Thr Cys Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Arg His Cys Cys
1 5 10 15Ser Gly Tyr Cys His Lys Thr Ile Gln Ala Cys Ser
20 25

<210> 317

<211> 33

<212> PRT

<213> Conus arenatus

<400> 317

Gln Cys Thr Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys
1 5 10 15Ser Leu Tyr Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Tyr
20 25 30

Pro

<210> 318

<211> 33

<212> PRT

<213> Conus arenatus

<400> 318

Gln Cys Thr Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys
1 5 10 15Ser Leu Tyr Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Tyr
20 25 30

Pro

<210> 319

<211> 27

<212> PRT

<213> Conus arenatus

<400> 319

Glu Cys Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys
1 5 10 15Gly Phe Cys Asp Thr Ala Asn Asn Arg Cys Leu
20 25

<210> 320

<211> 28

<212> PRT

<213> Conus arenatus

<400> 320

Thr Cys Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Gln His Cys Cys
1 5 10 15Ser Gly His Cys His Lys Thr Ile Gln Ala Cys Ala
20 25

<210> 321

<211> 30

<212> PRT

<213> Conus arenatus

<400> 321

Gln	Cys	Ser	Pro	Ile	Gly	Gly	Tyr	Cys	Thr	Leu	His	Ile	His	Cys	Cys
1				5				10				15			

Ser	Asn	His	Cys	Ile	Lys	Pro	Ile	Gly	Arg	Cys	Val	Ala	Thr		
				20				25				30			

<210> 322

<211> 30

<212> PRT

<213> Conus arenatus

<400> 322

Gln	Cys	Leu	Pro	Asn	Gly	Gly	Tyr	Cys	Thr	Leu	His	Ile	His	Cys	Cys
1				5				10				15			

Ser	Asp	His	Cys	Ile	Lys	Pro	Ile	Asp	Arg	Cys	Val	Ala	Thr		
				20				25				30			

<210> 323

<211> 25

<212> PRT

<213> Conus aurisiacus

<400> 323

Cys	Lys	Gly	Lys	Gly	Lys	Pro	Cys	Ser	Arg	Ile	Ser	Tyr	Asn	Cys	Cys
1				5				10				15			

Thr	Gly	Ser	Cys	Arg	Ser	Gly	Lys	Cys							
				20				25							

<210> 324

<211> 32

<212> PRT

<213> Conus aurisiacus

<400> 324

Cys	Met	Glu	Ala	Gly	Ser	Tyr	Cys	Gly	Ser	Thr	Thr	Arg	Ile	Cys	Cys
1				5				10				15			

Gly	Phe	Cys	Ala	Tyr	Phe	Gly	Lys	Lys	Cys	Ile	Asp	Tyr	Pro	Ser	Asn
				20				25				30			

<210> 325

<211> 25

<212> PRT

<213> Conus aurisiacus

<400> 325

Cys	Lys	Ala	Lys	Gly	Lys	Pro	Cys	Ser	Arg	Ile	Ala	Tyr	Asn	Cys	Cys
1				5				10				15			

Thr	Gly	Ser	Cys	Arg	Ser	Gly	Lys	Cys							
				20				25							

<210> 326

<211> 26

<212> PRT

<213> Conus aurisiacus

<400> 326
 Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn
 1 5 10 15

Ala Cys Asp Pro Gly Arg Asn Ile Cys Thr
 20 25

<210> 327
 <211> 36
 <212> PRT
 <213> Conus bullatus

<400> 327
 Ser Thr Ser Cys Met Glu Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr
 1 5 10 15

Lys Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Asn
 20 25 30

Asn Pro Asn Asn
 35

<210> 328
 <211> 31
 <212> PRT
 <213> Conus bullatus

<400> 328
 Cys Ile Thr Pro Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg
 1 5 10 15

Gly Pro Cys Lys Asn Gly Arg Cys Thr Pro Ser Pro Ser Glu Trp
 20 25 30

<210> 329
 <211> 26
 <212> PRT
 <213> Conus bullatus

<400> 329
 Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn
 1 5 10 15

Thr Cys Asp Pro Ala Arg Arg Thr Cys Thr
 20 25

<210> 330
 <211> 25
 <212> PRT
 <213> Conus bullatus

<400> 330
 Cys Lys Gly Pro Gly Ala Ser Cys Ile Arg Ile Ala Tyr Asn Cys Cys
 1 5 10 15

Lys Tyr Ser Cys Arg Asn Gly Lys Cys
 20 25

<210> 331
 <211> 36
 <212> PRT
 <213> Conus bullatus

<400> 331

Ser Thr Ser Cys Met Ala Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr
 1 5 10 15

Asn Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Lys
 20 25 30

Lys Pro Asn Asn
 35

<210> 332
 <211> 25
 <212> PRT
 <213> Conus bullatus

<400> 332
 Cys Lys Ser Lys Gly Ser Ser Cys His Arg Thr Ser Tyr Asp Cys Cys
 1 5 10 15

Thr Gly Ser Cys Arg Asn Gly Arg Cys
 20 25

<210> 333
 <211> 25
 <212> PRT
 <213> Conus catus

<400> 333
 Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Arg Cys
 20 25

<210> 334
 <211> 25
 <212> PRT
 <213> Conus catus

<400> 334
 Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys
 1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Ser Cys
 20 25

<210> 335
 <211> 28
 <212> PRT
 <213> Conus catus

<400> 335
 Cys Leu Pro Ala Gly Glu Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
 1 5 10 15

Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser
 20 25

<210> 336
 <211> 25
 <212> PRT
 <213> Conus catus

<400> 336
 Cys Gln Gly Arg Gly Gly Pro Cys Thr Lys Ala Val Phe Asn Cys Cys
 1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Arg Cys
20 25

<210> 337

<211> 26

<212> PRT

<213> Conus catus

<400> 337

Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn
1 5 10 15

Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr
20 25

<210> 338

<211> 25

<212> PRT

<213> Conus catus

<400> 338

Cys Arg Gly Arg Gly Gly Pro Cys Thr Lys Ala Met Phe Asn Cys Cys
1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Arg Cys
20 25

<210> 339

<211> 33

<212> PRT

<213> Conus characteristicus

<400> 339

Gln Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys
1 5 10 15

Ser Leu Tyr Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Tyr
20 25 30

Pro

<210> 340

<211> 26

<212> PRT

<213> Conus consors

<400> 340

Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn
1 5 10 15

Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr
20 25

<210> 341

<211> 25

<212> PRT

<213> Conus consors

<400> 341

Cys Lys Gly Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys

100

20

25

<210> 342
<211> 36
<212> PRT
<213> Conus consors

<400> 342
Ala Thr Asp Cys Ile Glu Ala Gly Asn Tyr Cys Gly Pro Thr Val Met
1 5 10 15

Lys Ile Cys Cys Gly Phe Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn
20 25 30

Tyr Pro Gln Asn
35

<210> 343
<211> 27
<212> PRT
<213> Conus catus

<400> 343
Cys Lys Gly Lys Gly Ala Ser Cys Thr Arg Leu Met Tyr Asp Cys Cys
1 5 10 15

His Gly Ser Cys Ser Ser Ser Lys Gly Arg Cys
20 25

<210> 344
<211> 25
<212> PRT
<213> Conus consors

<400> 344
Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys
1 5 10 15
Thr Gly Ser Cys Asn Arg Gly Lys Cys
20 25

<210> 345
<211> 26
<212> PRT
<213> Conus consors

<400> 345
Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn
1 5 10 15
Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr
20 25

<210> 346
<211> 25
<212> PRT
<213> Conus consors

<400> 346
Cys Lys Gly Thr Gly Lys Pro Cys Ser Arg Val Ala Tyr Asn Cys Cys
1 5 10 15
Thr Gly Ser Cys Arg Ser Gly Lys Cys
20 25

<210> 347

<211> 35
<212> PRT
<213> Conus consors

<400> 347
Ser Thr Ser Cys Met Lys Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg
1 5 10 15
Thr Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Phe Cys Ile Asp Phe
20 25 30

Pro Ser Asn
35

<210> 348
<211> 25
<212> PRT
<213> Conus circumcisus

<400> 348
Cys Lys Gly Lys Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys
1 5 10 15
Ser Gly Ser Cys Ser Asn Gly Arg Cys
20 25

<210> 349
<211> 35
<212> PRT
<213> Conus circumcisus

<400> 349
Ser Thr Ser Cys Met Glu Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg
1 5 10 15
Thr Cys Cys Gly Tyr Cys Ser Tyr Phe Ser Lys Lys Cys Ile Asp Phe
20 25 30

Pro Ser Asn
35

<210> 350
<211> 27
<212> PRT
<213> Conus circumcisus

<400> 350
Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys
1 5 10 15
Ser Gly Ser Cys Ser Arg Tyr Ser Gly Arg Cys
20 25

<210> 351
<211> 35
<212> PRT
<213> Conus circumcisus

<400> 351
Ser Thr Gly Cys Met Lys Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg
1 5 10 15
Thr Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr
20 25 30

Pro Ser Asn
 35

<210> 352
 <211> 28
 <212> PRT
 <213> Conus dalli

<400> 352
 Ser Cys Thr Pro Pro Gly Gly Pro Cys Gly Tyr Tyr Asn Asp Cys Cys
 1 5 10 15

Ser His Gln Cys Asn Ile Ser Arg Asn Lys Cys Glu
 20 25

<210> 353
 <211> 25
 <212> PRT
 <213> Conus distans

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa is Hyp

<400> 353
 Cys Glu Asp Xaa Gly Glu Xaa Cys Gly Ser Asp His Ser Cys Cys Gly
 1 5 10 15

Gly Ser Cys Asn His Asn Val Cys Ala
 20 25

<210> 354
 <211> 27
 <212> PRT
 <213> Conus ermineus

<400> 354
 Pro Cys Lys Pro Lys Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys
 1 5 10 15

Cys Asn Lys Thr Cys Thr Arg Ser Lys Cys Pro
 20 25

<210> 355
 <211> 27
 <212> PRT
 <213> Conus ermineus

<400> 355
 Ala Cys Trp Ser Ser Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys
 1 5 10 15

Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn
 20 25

<210> 356
 <211> 27
 <212> PRT
 <213> Conus geographus

<400> 356
 Cys Lys Ser Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys
 1 5 10 15

Arg Ser Cys Asn Pro Tyr Ala Lys Arg Cys Tyr
 20 25

<210> 357
 <211> 29
 <212> PRT
 <213> Conus geographus

<400> 357
 Cys Lys Ser Pro Gly Thr Pro Cys Ser Arg Gly Met Arg Asp Cys Cys
 1 5 10 15

Thr Pro Cys Leu Leu Tyr Ser Asn Lys Cys Arg Arg Tyr
 20 25

<210> 358
 <211> 30
 <212> PRT
 <213> Unknown

<220>
 <223> unknown Conus species

<400> 358
 Cys Leu Ser Pro Gly Ser Arg Cys His Lys Thr Met Arg Asn Cys Cys
 1 5 10 15

Thr Ser Cys Ser Ser Tyr Lys Gly Lys Cys Arg Pro Arg Lys
 20 25 30

<210> 359
 <211> 27
 <212> PRT
 <213> Unknown

<220>
 <223> unknown Conus species

<400> 359
 Cys Lys Pro Pro Gly Arg Lys Cys Leu Asn Arg Lys Asn Glu Cys Cys
 1 5 10 15

Ser Lys Phe Cys Asn Glu His Leu His Met Cys
 20 25

<210> 360
 <211> 26
 <212> PRT
 <213> Unknown

<220>
 <223> unknown Conus species

<400> 360
 Cys Lys Pro Pro Arg Arg Lys Cys Leu Lys Ile Lys Asp Lys Cys Cys
 1 5 10 15

Asn Phe Cys Asn Thr His Leu Asn Met Cys
 20 25

<210> 361
 <211> 28
 <212> PRT

<213> Unknown

<220>

<223> unknown Conus species

<400> 361

Cys	Ala	Gly	Pro	Gly	Thr	Ile	Cys	Pro	Asn	Arg	Val	Cys	Cys	Gly	Tyr
1															
			5					10							15

Cys	Ser	Lys	Arg	Thr	His	Leu	Cys	His	Ser	Arg	Thr
			20					25			

<210> 362

<211> 27

<212> PRT

<213> Conus laterculatus

<400> 362

Lys	Cys	Trp	Pro	Ser	Gly	Ser	Tyr	Cys	Arg	Ala	Asn	Ser	Lys	Cys	Cys
1															
				5				10							15

Ser	Gly	Cys	Asp	Arg	Asn	Arg	Asn	Lys	Cys	Tyr
			20					25		

<210> 363

<211> 27

<212> PRT

<213> Conus laterculatus

<400> 363

Cys	Leu	Pro	Pro	Gly	Ser	Tyr	Cys	Lys	Ala	Thr	Thr	Glu	Val	Cys	Cys
1															
				5				10							15

Ser	Ser	Cys	Leu	Gln	Phe	Ala	Gln	Ile	Cys	Ser
			20					25		

<210> 364

<211> 30

<212> PRT

<213> Conus lynceus

<400> 364

Cys	Lys	Ser	Pro	Gly	Ser	Pro	Cys	Ser	Val	Thr	Ser	Tyr	Asn	Cys	Cys
1															
				5					10						15

Thr	Phe	Cys	Ser	Ser	Tyr	Thr	Lys	Lys	Cys	Arg	Ala	Ser	Leu
			20					25					30

<210> 365

<211> 28

<212> PRT

<213> Conus lynceus

<400> 365

Cys	Ala	Gly	Pro	Gly	Ala	Ile	Cys	Pro	Asn	Arg	Val	Cys	Cys	Gly	Tyr
1															
				5					10						15

Cys	Ser	Lys	Arg	Thr	His	Leu	Cys	His	Ser	Arg	Thr
			20					25			

<210> 366

<211> 27

<212> PRT

<213> Conus lynceus

<400> 366
 Ala Cys Trp Ser Ser Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys
 1 5 10 15

Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn
 20 25

<210> 367

<211> 27

<212> PRT

<213> Conus lynceus

<400> 367

Lys Cys Trp Ser Pro Gly Thr Tyr Cys Arg Ala His Ser Lys Cys Cys
 1 5 10 15

Arg Gly Cys Asp Gln Asn Arg Asn Lys Cys Tyr
 20 25

<210> 368

<211> 29

<212> PRT

<213> Conus laterculatus

<400> 368

Cys Lys Ser Pro Gly Ser Ser Cys Ser Val Ser Met Arg Asn Cys Cys
 1 5 10 15

Thr Ser Cys Asn Ser Arg Thr Lys Lys Cys Thr Arg Arg
 20 25

<210> 369

<211> 27

<212> PRT

<213> Conus laterculatus

<400> 369

Thr Cys Trp Pro Ser Gly Thr Ala Cys Gly Ile Asp Ser Asn Cys Cys
 1 5 10 15

Ser Gly Cys Asn Val Ser Arg Ser Lys Cys Asn
 20 25

<210> 370

<211> 27

<212> PRT

<213> Conus laterculatus

<400> 370

Lys Cys Trp Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys
 1 5 10 15

Ser Gly Cys Asp Arg Asn Arg Ser Lys Cys Asn
 20 25

<210> 371

<211> 37

<212> PRT

<213> Conus leopardus

<400> 371

Ser Leu Phe Glu Cys Ala Pro Ser Gly Gly Arg Cys Gly Phe Leu Lys
 1 5 10 15

Ser Cys Cys Glu Gly Tyr Cys Asp Gly Glu Ser Thr Ser Cys Val Ser
 20 25 30

Gly Pro Tyr Ser Ile
 35

<210> 372
 <211> 30
 <212> PRT
 <213> Conus leopardus

<400> 372
 Trp Pro Leu Asp Cys Thr Ala Pro Ser Gln Pro Cys Gly Tyr Phe Pro
 1 . 5 10 15

Arg Cys Cys Gly His Cys Asp Val Arg Arg Val Cys Thr Ser
 20 25 30

<210> 373
 <211> 31
 <212> PRT
 <213> Conus leopardus

<400> 373
 Cys Met Ser Pro Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Glu
 1 . 5 10 15

Ile Cys Asn Val Tyr Gly Ile Cys Val Ser Asp Leu Pro Gly Ile
 20 25 30

<210> 374
 <211> 27
 <212> PRT
 <213> Conus leopardus

<400> 374
 Tyr Cys Ala Pro Pro Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys
 1 . 5 10 15

Gly Tyr Cys Glu Thr Phe Tyr Asn Thr Cys Arg
 20 25

<210> 375
 <211> 25
 <212> PRT
 <213> Conus magus

<400> 375
 Cys Lys Gly Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys
 1 . 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 376
 <211> 26
 <212> PRT
 <213> Conus magus

<400> 376
 Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn
 1 . 5 10 15

Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr
 20 25

<210> 377
<211> 27
<212> PRT
<213> Conus miles

<400> 377
Cys Asn Asp Arg Gly Gly Cys Ser Gln His Pro His Cys Cys Gly
1 5 10 15

Gly Thr Cys Asn Lys Leu Ile Gly Val Cys Leu
20 25

<210> 378
<211> 25
<212> PRT
<213> Conus monachus

<400> 378
Cys Lys Ser Thr Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
20 25

<210> 379
<211> 25
<212> PRT
<213> Conus monachus

<400> 379
Cys Lys Gly Lys Gly Ser Ser Cys Ser Arg Thr Met Tyr Asn Cys Cys
1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Lys Cys
20 25

<210> 380
<211> 35
<212> PRT
<213> Conus obscurus

<400> 380
Ser Pro Pro Cys Met Lys Gly Gly Ser Ser Cys Arg Gly Thr Thr Gly
1 5 10 15

Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Tyr Lys Cys Arg Asp Tyr
20 25 30

Pro Gln Asn
35

<210> 381
<211> 28
<212> PRT
<213> Conus obscurus

<400> 381
Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
1 . 5 10 15

Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
20 25

<210> 382

<211> 27
<212> PRT
<213> Conus purpurascens

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa is Hyp

<400> 382
Xaa Cys Lys Thr Xaa Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys
1 5 10 15
Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Pro
20 25

<210> 383
<211> 26
<212> PRT
<213> Conus purpurascens

<220>
<221> PEPTIDE
<222> (1)..(26)
<223> Xaa at residue 5 is Hyp; Xaa at residue 12 is gamma-carboxy-Glu

<400> 383
Ser Cys Lys Leu Xaa Gly Ala Tyr Cys Asn Ala Xaa Asp Tyr Asp Cys
1 5 10 15
Cys Leu Arg Cys Lys Val Gly Gly Thr Cys
20 25

<210> 384
<211> 27
<212> PRT
<213> Conus purpurascens

<400> 384
Pro Cys Lys Lys Thr Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys
1 5 10 15
Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Pro
20 25

<210> 385
<211> 30
<212> PRT
<213> Conus pulicarius

<400> 385
Gln Cys Ser Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys
1 5 10 15
Ser Leu Tyr Cys Asn Lys Asn Thr Gly Val Cys Ile Ala Thr
20 25 30

<210> 386
<211> 27
<212> PRT
<213> Conus pulicarius

<400> 386
Glu Cys Thr Pro Pro Asp Gly Ala Cys Gly Leu Pro Thr His Cys Cys
1 5 10 15

Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu
 20 25

<210> 387

<211> 27

<212> PRT

<213> Conus pulicarius

<400> 387

Glu Cys Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys
 1 5 10 15

Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu
 20 25

<210> 388

<211> 28

<212> PRT

<213> Conus radiatus

<400> 388

His Gly Cys Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys
 1 5 10 15

Cys Ser Lys Phe Cys Asn Ser Val Arg Lys Gln Cys
 20 25

<210> 389

<211> 28

<212> PRT

<213> Conus radiatus

<400> 389

Arg Gly Cys Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys
 1 5 10 15

Cys Ser Lys Phe Cys Asn Ser Val Arg Asn Gln Cys
 20 25

<210> 390

<211> 27

<212> PRT

<213> Conus rattus

<400> 390

Cys Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser
 1 5 10 15

Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
 20 25

<210> 391

<211> 27

<212> PRT

<213> Conus rattus

<400> 391

Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser
 1 5 10 15

Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
 20 25

<210> 392

<211> 27
<212> PRT
<213> Conus rattus

<400> 392
Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser
1 5 10 15
Gly Ser Cys Asn Lys Thr Leu Gly Val Cys Leu
20 25

<210> 393
<211> 34
<212> PRT
<213> Conus rattus

<400> 393
Ala Cys Thr Pro Glu Gly Ala Cys Ser Ser Gly Arg His Cys Cys
1 5 10 15
Gly Phe Cys Asp Asn Val Ser His Thr Cys Tyr Gly Glu Thr Pro Ser
20 25 30

Leu His

<210> 394
<211> 36
<212> PRT
<213> Conus striatus

<400> 394
Ala Thr Asp Cys Ile Glu Ala Gly Asn Tyr Cys Gly Pro Thr Val Met
1 5 10 15
Lys Ile Cys Cys Gly Phe Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn
20 25 30

Tyr Pro Lys Asn
35

<210> 395
<211> 26
<212> PRT
<213> Conus striatus

<400> 395
Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Tyr Asp Cys Cys
1 5 10 15
Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys
20 25

<210> 396
<211> 25
<212> PRT
<213> Conus striatus

<400> 396
Cys Lys Ala Ala Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
20 25

<210> 397

<211> 26

<212> PRT

<213> Conus striatus

<400> 397

Cys	Glu	Ser	Tyr	Gly	Lys	Pro	Cys	Gly	Ile	Tyr	Asn	Asp	Cys	Cys	Asn
1					5				10				15		

Ala	Cys	Asp	Pro	Ala	Lys	Lys	Thr	Cys	Thr						
							20		25						

<210> 398

<211> 27

<212> PRT

<213> Conus stercusmuscarum

<400> 398

Cys	Lys	Ser	Lys	Gly	Ala	Lys	Cys	Ser	Arg	Leu	Met	Tyr	Asp	Cys	Cys
1					5				10				15		

Ser	Gly	Ser	Cys	Ser	Gly	Tyr	Thr	Gly	Arg	Cys					
						20		25							

<210> 399

<211> 35

<212> PRT

<213> Conus stercusmuscarum

<400> 399

Thr	Thr	Ser	Cys	Met	Gln	Ala	Gly	Ser	Tyr	Cys	Gly	Ser	Thr	Thr	Arg
1				5					10				15		

Ile	Cys	Cys	Gly	Tyr	Cys	Ala	Tyr	Phe	Gly	Lys	Lys	Cys	Ile	Asp	Tyr
				20				25				30			

Pro	Ser	Asn													
		35													

<210> 400

<211> 26

<212> PRT

<213> Conus stercusmuscarum

<400> 400

Cys	Ala	Ser	Tyr	Gly	Lys	Pro	Cys	Gly	Ile	Asp	Asn	Asp	Cys	Cys	Asn
1					5				10				15		

Ala	Cys	Asp	Pro	Ala	Arg	Asn	Ile	Cys	Thr						
					20			25							

<210> 401

<211> 26

<212> PRT

<213> Conus stercusmuscarum

<400> 401

Cys	Val	Ser	Tyr	Gly	Lys	Pro	Cys	Gly	Ile	Asp	Asn	Asp	Cys	Cys	Asn
1					5				10				15		

Ala	Cys	Asp	Pro	Ala	Arg	Asn	Ile	Cys	Thr						
					20			25							

<210> 402

<211> 25

<212> PRT

<213> Conus stercusmuscarum

<400> 402
 Cys Lys Gly Lys Gly Ala Ser Cys His Lys Thr Met Tyr Asp Cys Cys
 1 5 10 15

Ser Gly Ser Cys Thr Arg Gly Arg Cys
 20 25

<210> 403
 <211> 25
 <212> PRT
 <213> Conus striolatus

<400> 403
 Cys Lys Gly Lys Gly Ala Ser Cys Leu Arg Thr Ala Tyr Asp Cys Cys
 1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Arg Cys
 20 25

<210> 404
 <211> 24
 <212> PRT
 <213> Conus striolatus

<400> 404
 Cys Arg Pro Ser Gly Ser Asn Cys Gly Asn Ile Ser Ile Cys Cys Gly
 1 5 10 15

Arg Cys Val Asn Arg Arg Cys Thr
 20

<210> 405
 <211> 35
 <212> PRT
 <213> Conus striolatus

<400> 405
 Ser Thr Ser Cys Met Lys Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg
 1 5 10 15

Ile Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Ile Cys Ile Asp Tyr
 20 25 30

Pro Lys Asn
 35

<210> 406
 <211> 28
 <212> PRT
 <213> Conus textile

<400> 406
 Tyr Cys Thr Pro His Gly Gly His Cys Gly Tyr His Asn Asp Cys Cys
 1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu
 20 25

<210> 407
 <211> 31
 <212> PRT
 <213> Conus viola

<400> 407

Cys Ile Thr Leu Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg
 1 5 10 15

Ser Ser Cys Lys Asn Gly Arg Cys Ala Pro Ser Pro Glu Glu Trp
 20 25 30

<210> 408

<211> 25

<212> PRT

<213> Conus viola

<400> 408

Cys Lys Ser Arg Gly Ser Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys
 1 5 10 15

Thr Gly Ser Cys Arg Asn Gly Lys Cys
 20 25

<210> 409

<211> 36

<212> PRT

<213> Conus viola

<400> 409

Ser Thr Ser Cys Met Glu Ala Arg Ser Tyr Cys Gly Pro Ala Thr Thr
 1 5 10 15

Lys Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Asn
 20 25 30

Asn Pro Asn Asn

35

<210> 410

<211> 25

<212> PRT

<213> Conus viola

<400> 410

Cys Lys Gly Pro Gly Ala Ile Cys Ile Arg Ile Ala Tyr Asn Cys Cys
 1 5 10 15

Lys Tyr Ser Cys Gly Asn Gly Lys Cys
 20 25

<210> 411

<211> 28

<212> PRT

<213> Conus viola

<400> 411

Tyr Cys Thr Pro Tyr Gly Gly His Cys Gly Tyr Tyr Asn Asp Cys Cys
 1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu
 20 25

<210> 412

<211> 27

<212> PRT

<213> Conus textile

<400> 412

Cys Thr Pro Tyr Gly Gly His Cys Gly Tyr Asn His Asp Cys Cys Ser
1 5 10 15

His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu
20 25

<210> 413
<211> 26
<212> PRT
<213> Conus tulipa

<220>
<221> PEPTIDE
<222> (1)..(26)
<223> Xaa is Hyp

<400> 413
Cys Lys Ser Trp Gly Ser Xaa Cys Ser Xaa Thr Ser Thr Asn Cys Cys
1 5 10 15

Trp Ser Cys Ser Pro Tyr Arg Lys Lys Cys
20 25